

GenCore version 4.5
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CM protein - protein search, using sw model

Run on: December 13, 1999, 02:19:50 ; Search time 29.27 Seconds

(without alignments)
323.691 Million cell updates/sec

Title: US-09-272-835-15

Perfect score: 2190

Sequence: 1 MVRPLNRPPLPVVLMILL.....PMVPSLFSCTLPILLISIM 400

Scoring table: BLOSUM62

Searched: 188963 seqs, 23686106 residues

Abase: A_Geneseq_36.*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2190	100.0	400	1	W37463	Human Ret ligand R
2	2190	100.0	400	1	W65116	Human GDNF alpha-3
3	2190	100.0	400	1	W84186	Glia1 cell line-de
4	2186	99.8	400	1	W84180	A GDNFR-alpha-rela
5	2184	99.7	400	1	W65117	Human GDNF alpha-3
6	2043	93.3	378	1	W84185	Glia1 cell line-de
7	1708	78.0	315	1	W37462	Human Ret ligand R
8	1646.5	75.2	397	1	W37461	Mouse Ret ligand R
9	1642.5	75.0	397	1	W84182	A GDNFR-alpha-rela
10	1455	66.4	346	1	W37465	Mouse Ret ligand R
11	944	43.1	172	1	W65118	Human GDNF alpha-3
12	632.5	28.9	498	1	W84183	Consensus sequence
13	589.5	26.9	489	1	W84298	A GDNFR-alpha-rela
14	547.5	25.0	460	1	W84181	Mouse TGF-beta rel
15	544.5	24.9	463	1	W81624	Mouse mature TGF-b
16	544.5	24.9	411	1	W81625	Rat mature TGF-b
17	542.5	24.8	664	1	W71604	Rat neurturin rece
18	542.5	24.8	464	1	W71602	Rat neurturin rece
19	542.5	24.8	464	1	W92299	Rat GDNFR-beta pol
20	540.5	24.7	464	1	W37460	Human Ret ligand R
21	540.5	24.7	464	1	W71601	Human neurturin re
22	540.5	24.7	464	1	W71603	Human neurturin re
23	540.5	24.7	464	1	W81622	Human TGF-beta rel
24	540.5	24.7	411	1	W81623	Human mature TGF-b
25	540.5	24.7	464	1	W84184	Glia1 cell line-de
26	540.5	24.7	464	1	W84179	A GDNFR-alpha-rela
27	540.5	24.7	464	1	W92301	Human GDNFR-beta P
28	517.5	23.6	460	1	W37459	Human Ret ligand R
29	516	23.6	465	1	W35333	Human Glia1 cell, 1
30	516	23.6	465	1	W84163	Glia1 cell line-de
31	516	23.6	463	1	W84166	GDNFR-alpha protei
32	516	23.6	463	1	W84167	Human GDNFR-alpha
33	516	23.6	465	1	W92300	Human GDNFR-alpha
34	515	23.5	465	1	W81665	GDNFR-alpha protei
35	511	23.3	468	1	W27327	Rat Glia1 cell der
36	511	23.3	468	1	W35334	Rat Glia1 cell lin
37	511	23.3	468	1	W37457	Rat Ret ligand Ret
38	511	23.3	468	1	W84164	Glia1 cell line-de
39	504	23.0	468	1	W92298	Rat GDNFR-alpha po
40	405	18.5	330	1	W81627	Mouse TGF-beta rel
41	401	18.3	331	1	W81626	Human TGF-beta rel
42	389.5	17.8	346	1	W37458	Human Ret ligand R
43	336.5	15.4	232	1	W84168	GDNFR-alpha protei

ALIGNMENTS

44 336.5 15.4 294 1 W84169 GDNFR-alpha protei
45 210 9.6 219 1 W84170 GDNFR-alpha protei

RESULT 1

W37463 standard; Protein; 400 AA.
ID W37463;
AC W37463;
DE 21-MAY-1998 (first entry)
KW Human Ret ligand Ret3.
KW Ret ligand; Ret3; Ret3; receptor; signal transduction; human;
KW cell growth; renal cell; nerve cell; renal failure; nephritis;
KW kidney transplant; toxic injury; hypoxic injury;
KW neurodegeneration; motor neurone disease; multiple sclerosis;
KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
KW cranial nerve injury; spinal cord injury; Down's syndrome;
KW cerebral palsy; Lyme disease; muscular dystrophy;
KW myasthenia gravis; tumour; therapy.
OS Homo sapiens.
PN M09744336-A2
PF 07-MAY-1997; U07726.
PR 10-APR-1997; US-017427.
PR 08-MAY-1996; US-017427.
PR 07-JUN-1996; US-019300.
PR 16-JUL-1996; US-021859.
PA (Bio) BIOGEN INC.
PI Cate RL, Hession C, Santicola-Nadel M;
DR W84182; W00251.
DR N-PSDB; V00251.
PT New nucleic acid encoding ret receptor ligands and related proteins
PT -vectors, transformed cells and antibodies, used for promoting cell
PT growth and improving survival of injured cells, especially renal or
PT nerve cells.
PS Claim 2: Page 85-86; 113P: English.
CC This amino acid sequence comprises human Ret ligand (Ret), Ret3,
CC deduced from cDNA clones (see V00251) isolated from a adult heart
CC and spinal cord libraries. Rat and human Ret3, human Ret2 and
CC mouse Ret3 sequences (see W37457-62) are also claimed. Human
CC Ret3 is 34.3% identical to human Ret3, 34.9% identical to human
CC Ret2 and 76.8% identical to murine Ret3. Ret ligand is a key
CC component of the Ret signalling pathway that specifically
CC interacts with Ret receptor protein, triggering Ret dimetrisation
CC and/or autophosphorylation of the Ret tyrosine kinase domain.
CC Vectors containing Ret3 DNA and prokaryotic or eukaryotic host
CC cells transfected or transfected with these vectors are claimed, as
CC well as a method for production of Ret3. Its soluble variants and
CC fusion proteins with a toxin, imageable compound or radionuclide.
CC Ret3, optionally when expressed from vectors in vivo, is used to
CC promote growth of new tissue and survival of damaged tissue,
CC particularly kidney or neural tissue. Typical applications are in
CC renal failure, nephritis, kidney transplants, toxic or hypoxic
CC injury, neurodegeneration, motor neurone disease, multiple sclerosis,
CC associated with HIV or prion infections (e.g. meningitis, myelopathy
CC and spinal cord injury, developmental disorders such as Down's syndrome
CC and cerebral palsy, or conditions involving the peripheral nervous
CC system (Lyme disease, muscular dystrophy and myasthenia gravis).
CC Fusion proteins are used to deliver toxins etc. to Ret-expressing
CC cells, especially tumours.
SO Sequence 400 AA.

Query Match 100.0%; Score 2190; DB 1; Length 400;

Best Local Similarity 100.0%; Pred. No. 5.8e-188;

Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y 1 MVRPLNRPPLPVVLMILLIPSPPLAAGDPLTESRLMNSCLARRKCAADPTCSAA 60
DB 1 MVRPLNRPPLPVVLMILLIPSPPLAAGDPLTESRLMNSCLARRKCAADPTCSAA 60

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OY 61 YHLDSCSTSSITPLPSEEPSPADCLAAOOLRNSSLIGCMCHRRMKNOVACLDIYTV 120
DB 61 YHLDSCSTSSITPLPSEEPSPADCLAAOOLRNSSLIGCMCHRRMKNOVACLDIYTV 120
OY 121 HARSISGNELDVSPYEDTVTSKPMKMLSKLNMKRPDSCLKFMCTLNDKCDRLK 180
DB 121 HARSISGNELDVSPYEDTVTSKPMKMLSKLNMKRPDSCLKFMCTLNDKCDRLK 180
OY 181 AYGEACSGPHCRHVCRLQLLTFFEKAAEPHAQGLLPCAPNDRCGERRRNTIAPNCA 240
DB 181 AYGEACSGPHCRHVCRLQLLTFFEKAAEPHAQGLLPCAPNDRCGERRRNTIAPNCA 240
OY 241 LPPVAPNCLERLRCFSDPLCRSLVDFTCHHPMDILGTCTEORSCLRAYLGLIGTAM 300
DB 241 LPPVAPNCLERLRCFSDPLCRSLVDFTCHHPMDILGTCTEORSCLRAYLGLIGTAM 300
OY 301 TPNEFSNNTSVALSCTCRSGNLOECCMELEGGFESHNPCLTEAIAAKRRHSOLFSDM 360
DB 301 TPNEFSNNTSVALSCTCRSGNLOECCMELEGGFESHNPCLTEAIAAKRRHSOLFSDM 360
OY 361 PPHTEFAVAHONENPAVRPQWPVPSLFCSTLPLILLSLM 400
DB 361 PPHTEFAVAHONENPAVRPQWPVPSLFCSTLPLILLSLM 400

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RESULT 2

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ID W65116 standard; Protein; 400 AA.
AC W65116;
DE Human GDNF alpha-3 receptor protein #1.
KW Glial cell line-derived neurotrophic factor alpha-3 receptor; GDNF;
KW treatment; neurodegenerative disease; Parkinson's disease; ALS; SMA;
KW amyotrophic lateral sclerosis; spinal muscular atrophy; nerve; trauma;
KW Huntington's disease; Alzheimer's disease; diabetic neuropathy; muscle;
KW muscular dystrophy; diagnostic.
OS Homo sapiens.
FH Key
FT Location/Qualifiers
FT 1..400
FT /label= "GDNF alpha-3"
FT /note= "Partial sequence"
PD EP-846764-A2.
PD 10-SEP-1998
PD 20-NOV-1997; 309375.
PR 09-MAY-1997; GB-009463.
PR 27-NOV-1996; GB-024677.
PA (SWIK) SMITHKLINE BEECHAM PLC.
LA Lawrence GMP;
FT MPI; 98-239980/27.
FT N-PSDB; V35364.
PT New factor alpha 3 receptor polypeptide and e.g. DNA and agonists -
PT used to treat neuro degenerative diseases, muscular diseases and
PT nerve and muscle trauma and in diagnostic assays
PS Claim 4; Fig 2; 22pp; English.
CC This sequence represents a novel glial cell line-derived neurotrophic
CC factor alpha-3 receptor (GDNF alpha-3). This protein can be used to
CC treat e.g. neurodegenerative diseases (such as Parkinson's disease,
CC amyotrophic lateral sclerosis (ALS), spinal muscular atrophy (SMA),
CC Huntington's disease, Alzheimer's disease, diabetic neuropathy),
CC muscular diseases (including the muscular dystrophies) and nerve and
CC muscle trauma and in diagnostic assays for such conditions.
SO Sequence 400 AA;

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Query Match 100.0%; Score 2190; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 5.8e-188;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 WVRPLNPRLPVPVIMLLLPSPSLPLAAGDPLTERLNKSCIQARRKKQADPTCSAA 60
DB 1 WVRPLNPRLPVPVIMLLLPSPSLPLAAGDPLTERLNKSCIQARRKKQADPTCSAA 60

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OY 61 YHLDSCSTSSITPLPSEEPSPADCLAAOOLRNSSLIGCMCHRRMKNOVACLDIYTV 120
DB 61 YHLDSCSTSSITPLPSEEPSPADCLAAOOLRNSSLIGCMCHRRMKNOVACLDIYTV 120
OY 121 HARSISGNELDVSPYEDTVTSKPMKMLSKLNMKRPDSCLKFMCTLNDKCDRLK 180
DB 121 HARSISGNELDVSPYEDTVTSKPMKMLSKLNMKRPDSCLKFMCTLNDKCDRLK 180
OY 181 AYGEACSGPHCRHVCRLQLLTFFEKAAEPHAQGLLPCAPNDRCGERRRNTIAPNCA 240
DB 181 AYGEACSGPHCRHVCRLQLLTFFEKAAEPHAQGLLPCAPNDRCGERRRNTIAPNCA 240
OY 241 LPPVAPNCLERLRCFSDPLCRSLVDFTCHHPMDILGTCTEORSCLRAYLGLIGTAM 300
DB 241 LPPVAPNCLERLRCFSDPLCRSLVDFTCHHPMDILGTCTEORSCLRAYLGLIGTAM 300
OY 301 TPNEFSNNTSVALSCTCRSGNLOECCMELEGGFESHNPCLTEAIAAKRRHSOLFSDM 360
DB 301 TPNEFSNNTSVALSCTCRSGNLOECCMELEGGFESHNPCLTEAIAAKRRHSOLFSDM 360
OY 361 PPHTEFAVAHONENPAVRPQWPVPSLFCSTLPLILLSLM 400
DB 361 PPHTEFAVAHONENPAVRPQWPVPSLFCSTLPLILLSLM 400

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RESULT 3

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ID W84186 standard; Protein; 400 AA.
AC W84186;
DE 25-MAR-1999 (first entry)
DE Glial cell line-derived neurotrophic factor receptor gamma 2.
KW Glial cell line-derived neurotrophic factor receptor gamma 2;
KW GDNFR-alpha; glial cell line-derived neurotrophic factor; GDNF;
KW neurodegenerative disease; amyotrophic lateral sclerosis; GDNFR-gamma2;
KW Parkinson's disease; schizophrenia; insomnia; tardive dyskinesia;
KW hypertension; pituitary adenomas; hyperprolactinemia; thyroid tumour;
KW renal disorder; kidney failure; gut dysfunction; regeneration;
KW cardiomyocyte; epithelium; hepatocyte.
OS Homo sapiens.
FH Key
FT Location/Qualifiers
FT 1..31
FT /label= "Peptide"
FT 32..400
FT /label= "signal-peptide"
FT Protein
FT 32..400
FT /label= "mature-protein"
FT Domain
FT 32..382
FT /note= "extracellular domain"
FT 383..400
FT /note= "transmembrane domain"
PD M09B51056-A2.
PD 26-NOV-1998
PD 20-MAY-1998; U10328.
PR 27-JUN-1997; US-884638.
PR 20-MAY-1997; US-047092.
PA (HUMA-) HDMAN GENOME SCI INC.
PI Gentz RL, Hsu T, Ni J, Ruben SM, Young P;
DR MPI; 99-070150/06.
DR N-PSDB; V93934.
PT New isolated glial cell derived neurotrophic factor receptors - used
PT to develop products for treating e.g. neurodegenerative disorders,
PT schizophrenia, hypertension, tumours, renal disorders, kidney
PT failure or gut dysfunction
PS Claim 53; Fig 7A-D; 16pp; English.
CC The present sequence represents a glial cell line-derived neurotrophic
CC factor receptor gamma 2 (GDNFR-gamma2). GDNFR-gamma2 shares high homology
CC with GDNFR-alpha, which is capable of complexing with glial cell
CC line-derived neurotrophic factor (GDNF) and mediating cell response to
CC GDNF. The GDNFR polypeptides and agonists can be used for treating
CC disorders associated with decreased activity of the respective
CC polypeptides. They can be used for treating neurodegenerative diseases
CC such as amyotrophic lateral sclerosis, Parkinson's disease,
CC schizophrenia, insomnia, tardive dyskinesia, hypertension, pituitary
CC adenomas, hyperprolactinemia, thyroid tumour, renal disorders, kidney
CC failure, gut dysfunction, or for regeneration of cardiomyocytes,

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CC epithelium or hepatocytes. Antagonists of the polypeptides can be used
 CC for treating disorders associated with increased activity of the
 CC respective polypeptides. The products can also be used for detection,
 CC diagnosis and drug screening.
 SQ Sequence 400 AA;

Query Match 100.0%; Score 2190; DB 1; Length 400;
 Best Local Similarity 100.0%; Pred. No. 5,8e-188;
 Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYRLNRPPLPPVYLMILLPLPSPLPLAAGDPLTESRLMNSCLQARRRQADPTCSAA 60
 DB 1 MYRLNRPPLPPVYLMILLPLPSPLPLAAGDPLTESRLMNSCLQARRRQADPTCSAA 60
 QY YHHDSCSTSSISTPLPSEEPSVPADCLEAAQOLRNSSLIGCMCHRRKNQVACDIYTV 120
 DB YHHDSCSTSSISTPLPSEEPSVPADCLEAAQOLRNSSLIGCMCHRRKNQVACDIYTV 120
 QY 121 HRAASLGNELDVSPYEDYTSKPMKNLSKLNMLKPSDCLCFAMLCITLNDKDLRK 180
 DB 121 HRAASLGNELDVSPYEDYTSKPMKNLSKLNMLKPSDCLCFAMLCITLNDKDLRK 180
 QY 181 AYGACGPGHQRHVCRLQLLTFEKAEPHAQGLLCPAPNDRGGERRRNTIAPNCA 240
 DB 181 AYGACGPGHQRHVCRLQLLTFEKAEPHAQGLLCPAPNDRGGERRRNTIAPNCA 240
 QY 241 LPPVAPNCLERLRCFSDPLCRSLVDFOYHCHPMDLTGTCATEQSRLRAYLGLIGTAM 300
 DB 241 LPPVAPNCLERLRCFSDPLCRSLVDFOYHCHPMDLTGTCATEQSRLRAYLGLIGTAM 300
 QY 301 TPNFVSNVNTSVASCRCRSGNLQEECEMLEGFFSHNPCLTEAIAAKMRHSOLFSDM 360
 DB 301 TPNFVSNVNTSVASCRCRSGNLQEECEMLEGFFSHNPCLTEAIAAKMRHSOLFSDM 360
 QY 361 PHPTFAVMAHONENPAPVPOWPVPSLFSCTPLILLISLM 400
 DB 361 PHPTFAVMAHONENPAPVPOWPVPSLFSCTPLILLISLM 400

RESULT 4

W64180 standard; Protein; 400 AA.
 AC W64180;
 DT 25-MAR-1999 (first entry)
 DE A GDNFR-alpha-related protein 3 (GRR3).
 KW Human; glial cell-line derived neurotrophic factor receptor;
 KW GDNFR; glial cell line-derived neurotrophic factor; GDNF;
 KW neurturin; signal transduction; dopaminergic nerve cell;
 KW Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;
 KW neurological disorder; diabetes; glaucoma; sensory neuron;
 KW retinal ganglion cell degeneration; sensory neuropathy;
 KW retinopathy; gene therapy; GDNFR-related protein 3; GRR3.
 OS Homo sapiens.
 PN W09844213-A2.
 PF 03-DEC-1998;
 PR 27-APR-1998; U08486.
 PR 30-MAY-1997; US-866354.
 PA (AMGE-) AMGEN INC.
 PI Fox GM, Jling S, Wen D;
 DR WPI-98-080806/07.
 DR N-PSDB; V99329.
 PT New isolated glial cell line-derived neurotrophic factor receptors -
 PT used to develop products for treating e.g. improperly functioning
 PT dopaminergic nerve cells, Parkinson's disease, Alzheimer's disease
 PT or amyotrophic lateral sclerosis
 PS Claim 51; Fig 15; 318pp; English.
 CC The present sequence represents a human glial cell-line derived
 CC neurotrophic factor receptor (GDNFR)-related protein 3 (GRR3).
 CC The protein has similar functions to GDNFR. GDNFR proteins are
 CC functionally characterised by the ability to bind glial cell
 CC line-derived neurotrophic factor (GDNF) and/or neurturin specifically,
 CC and to act as part of a molecular complex which mediates or enhances

CC the signal transduction affects of GDNF and/or neurturin. The proteins
 CC can be used for treating improperly functioning dopaminergic nerve
 CC cells, Parkinson's disease, Alzheimer's disease or amyotrophic lateral
 CC sclerosis. They can also be used for treating neurological disorders
 CC associated with diabetes, glaucoma or other diseases and conditions
 CC involving retinal ganglion cell degeneration, sensory neuropathy caused
 CC by injury to, insults to, or degeneration of, sensory neurons,
 CC pathological conditions, or disease or injury-related retinopathies.
 CC The products can also be used for detection, diagnosis, drug screening
 CC and gene therapy.
 SQ Sequence 400 AA;

Query Match 99.8%; Score 2186; DB 1; Length 400;
 Best Local Similarity 99.8%; Pred. No. 1.3e-187;
 Matches 399; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MYRLNRPPLPPVYLMILLPLPSPLPLAAGDPLTESRLMNSCLQARRRQADPTCSAA 60
 DB 1 MYRLNRPPLPPVYLMILLPLPSPLPLAAGDPLTESRLMNSCLQARRRQADPTCSAA 60
 QY YHHDSCSTSSISTPLPSEEPSVPADCLEAAQOLRNSSLIGCMCHRRKNQVACDIYTV 120
 DB YHHDSCSTSSISTPLPSEEPSVPADCLEAAQOLRNSSLIGCMCHRRKNQVACDIYTV 120
 QY 61 YHHDSCSTSSISTPLPSEEPSVPADCLEAAQOLRNSSLIGCMCHRRKNQVACDIYTV 120
 DB 61 YHHDSCSTSSISTPLPSEEPSVPADCLEAAQOLRNSSLIGCMCHRRKNQVACDIYTV 120
 QY 121 HRAASLGNELDVSPYEDYTSKPMKNLSKLNMLKPSDCLCFAMLCITLNDKDLRK 180
 DB 121 HRAASLGNELDVSPYEDYTSKPMKNLSKLNMLKPSDCLCFAMLCITLNDKDLRK 180
 QY 181 AYGACGPGHQRHVCRLQLLTFEKAEPHAQGLLCPAPNDRGGERRRNTIAPNCA 240
 DB 181 AYGACGPGHQRHVCRLQLLTFEKAEPHAQGLLCPAPNDRGGERRRNTIAPNCA 240
 QY 241 LPPVAPNCLERLRCFSDPLCRSLVDFOYHCHPMDLTGTCATEQSRLRAYLGLIGTAM 300
 DB 241 LPPVAPNCLERLRCFSDPLCRSLVDFOYHCHPMDLTGTCATEQSRLRAYLGLIGTAM 300
 QY 301 TPNFVSNVNTSVASCRCRSGNLQEECEMLEGFFSHNPCLTEAIAAKMRHSOLFSDM 360
 DB 301 TPNFVSNVNTSVASCRCRSGNLQEECEMLEGFFSHNPCLTEAIAAKMRHSOLFSDM 360
 QY 361 PHPTFAVMAHONENPAPVPOWPVPSLFSCTPLILLISLM 400
 DB 361 PHPTFAVMAHONENPAPVPOWPVPSLFSCTPLILLISLM 400

RESULT 5

W65117 standard; Protein; 400 AA.
 AC W65117;
 DT 28-SEP-1998 (first entry)
 DE Human GDNF alpha-3 receptor protein #2.
 KW Glial cell line-derived neurotrophic factor alpha-3 receptor; GDNF;
 KW treatment; neurodegenerative disease; Parkinson's disease; SMA;
 KW amyotrophic lateral sclerosis; spinal muscular atrophy; nerve trauma;
 KW Huntington's Disease; Alzheimer's Disease; diabetic neuropathy; muscle;
 KW muscular dystrophy; diagnostic.
 OS Homo sapiens.
 PN Key
 FT Location/Qualifiers
 FT 1..400
 FT /label= GDNF alpha-3
 FT /note= "Partial sequence"
 EP-846764-A2.
 PD 10-JUN-1998.
 PD 26-NOV-1997; 309375.
 PR 09-MAY-1997; GB-009463.
 PR 27-NOV-1996; GB-024677.
 PA (SMK) SMITHKLINE BEECHAM PLC.
 PI Lawrence GMP;
 DR WPI: 98-299980/27.
 DR N-PSDB; V35365.
 PT New factor alpha 3 receptor polypeptide and e.g. DNA and agonists -
 PT used to treat neuro degenerative diseases, muscular diseases and

PT nerve and muscle trauma and in diagnostic assays
 PS claim 13; fig 4; 22pp; English.
 CC This sequence represents a novel glial cell line-derived neurotrophic
 CC factor alpha-3 receptor (GDNF alpha-3). This protein can be used to
 CC treat e.g. neurodegenerative diseases (such as Parkinson's disease,
 CC Huntington's disease, Alzheimer's disease, diabetic neuropathy),
 CC muscular diseases (including the muscular dystrophies) and nerve and
 CC muscle trauma and in diagnostic assays for such conditions.
 SQ Sequence 400 AA;

Query Match 99.7%; Score 2184; DB 1; Length 400;
 Best Local Similarity 99.8%; Pred. No. 2e-187;
 Matches 399; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MYRPLNRPPLPVVYMLLLLPSPPLAAGDPLTESRLMNSCLQARRKQADPTCSAA 60
 DB 1 MYRPLNRPPLPVVYMLLLLPSPPLAAGDPLTESRLMNSCLQARRKQADPTCSAA 60
 61 YHHLDSCTSSISTPPLSEPSVPADCLEAAQOLRNSSLIGCMCHRRMKNQVACLDIYWTY 120
 DB 61 YHHLDSCTSSISTPPLSEPSVPADCLEAAQOLRNSSLIGCMCHRRMKNQVACLDIYWTY 120
 QY 121 HRRASLGNYELDVSPYEDVTYSKPKMNLKPSDCLKFMALCTLNDKCDRLRK 180
 DB 121 HRRASLGNYELDVSPYEDVTYSKPKMNLKPSDCLKFMALCTLNDKCDRLRK 180
 QY 181 AYGEACSGPHCQRHVCRLQLLTFEKAEPHAGLLCPCAPNDGCGERRNTIAPNCA 240
 DB 181 AYGEACSGPHCQRHVCRLQLLTFEKAEPHAGLLCPCAPNDGCGERRNTIAPNCA 240
 QY 241 LPPVAPNCLERLRCFSDPLCRSLVDFTQCHPMDLIGTCATEQSRLRAYLIGITAM 300
 DB 241 LPPVAPNCLERLRCFSDPLCRSLVDFTQCHPMDLIGTCATEQSRLRAYLIGITAM 300
 QY 301 TPNFVSNNTSVALLSCTCRSGNLADECEMLEGFFSHNPLCTEALAAKRRHSOLFSDW 360
 DB 301 TPNFVSNNTSVALLSCTCRSGNLADECEMLEGFFSHNPLCTEALAAKRRHSOLFSDW 360
 QY 361 PPTFAVAHAQNNENPAVRPQWPVPSLFSCTPLILLISLM 400
 DB 361 PPTFAVAHAQNNENPAVRPQWPVPSLFSCTPLILLISLM 400
 RESULT 6
 W84185
 W84185 standard; Protein; 378 AA.
 25-MAR-1999 (first entry)
 DE glial cell line-derived neurotrophic factor receptor gamma 1;
 KW glial cell line-derived neurotrophic factor receptor gamma 1;
 KW GDNFR-alpha; glial cell line-derived neurotrophic factor; GDNF;
 KW neurodegenerative disease; amyotrophic lateral sclerosis; GDNFR-gamma1;
 KW Parkinson's disease; schizophrenia; insomnia; tardive dyskinesia;
 KW hypertension; pituitary adenomas; hyperprolactinemia; thyroid tumour;
 KW renal disorder; kidney failure; gut dysfunction; regeneration;
 KW cardiomyocyte; epithelium; hepatocyte.
 OS Homo sapiens.
 FH Key
 FT Peptide 1..31
 FT /label- signal_peptide
 FT /label- mature_protein
 FT /label- mature_protein
 FT /note- "extracellular domain"
 FT /note- "transmembrane domain"
 FT /note- "transmembrane domain"
 PN Domain
 PD 26-NOV-1998.
 PF 20-MAY-1998; U10328.
 PR 27-JUN-1997; US-884638.
 PR 20-MAY-1997; US-047092.

PA (HOMA-) HUMAN GENOME SCT INC.
 PI Gentz RL, Hsu T, Ni J, Ruben SM, Young P;
 DR WPI; 99-070150/06.
 DR N-PSDB; V99333.
 PT New isolated glial cell derived neurotrophic factor receptors - used
 PT to develop products for treating e.g. neurodegenerative disorders,
 PT schizophrenia, hypertension, tumours, renal disorders, kidney
 PT failure or gut dysfunction
 PS Claim 26; fig 4A-C; 156pp; English.
 CC The present sequence represents a glial cell line-derived neurotrophic
 CC factor receptor gamma 1 (GDNFR-gamma1). GDNFR-gamma1 shares high homology
 CC with GDNFR-alpha, which is capable of complexing with glial cell
 CC line-derived neurotrophic factor (GDNF) and mediating cell response to
 CC GDNF. The GDNFR polypeptides and agonists can be used for treating
 CC disorders associated with decreased activity of the respective
 CC polypeptides. They can be used for treating neurodegenerative diseases
 CC such as amyotrophic lateral sclerosis, Parkinson's disease,
 CC schizophrenia, insomnia, tardive dyskinesia, hypertension, pituitary
 CC adenomas, hyperprolactinemia, thyroid tumour, renal disorders, kidney
 CC failure, gut dysfunction, or for regeneration of cardiomyocytes,
 CC epithelium or hepatocytes. Antagonists of the polypeptides can be used
 CC for treating disorders associated with increased activity of the
 CC respective polypeptides. The products can also be used for detection,
 CC diagnosis and drug screening.
 SQ Sequence 378 AA;

Query Match 93.3%; Score 2043; DB 1; Length 378;
 Best Local Similarity 94.5%; Pred. No. 7.4e-175;
 Matches 378; Conservative 0; Mismatches 0; Indels 22; Gaps 1;

QY 1 MYRPLNRPPLPVVYMLLLLPSPPLAAGDPLTESRLMNSCLQARRKQADPTCSAA 60
 DB 1 MYRPLNRPPLPVVYMLLLLPSPPLAAGDPLTESRLMNSCLQARRKQADPTCSAA 60
 61 YHHLDSCTSSISTPPLSEPSVPADCLEAAQOLRNSSLIGCMCHRRMKNQVACLDIYWTY 120
 DB 61 YHHLDSCTSSISTPPLSEPSVPADCLEAAQOLRNSSLIGCMCHRRMKNQVACLDIYWTY 120
 QY 121 HRRASLGNYELDVSPYEDVTYSKPKMNLKPSDCLKFMALCTLNDKCDRLRK 180
 DB 121 HRRASLGNYELDVSPYEDVTYSKPKMNLKPSDCLKFMALCTLNDKCDRLRK 180
 QY 181 AYGEACSGPHCQRHVCRLQLLTFEKAEPHAGLLCPCAPNDGCGERRNTIAPNCA 240
 DB 181 AYGEACSGPHCQRHVCRLQLLTFEKAEPHAGLLCPCAPNDGCGERRNTIAPNCA 240
 QY 241 LPPVAPNCLERLRCFSDPLCRSLVDFTQCHPMDLIGTCATEQSRLRAYLIGITAM 300
 DB 241 LPPVAPNCLERLRCFSDPLCRSLVDFTQCHPMDLIGTCATEQSRLRAYLIGITAM 300
 QY 301 TPNFVSNNTSVALLSCTCRSGNLADECEMLEGFFSHNPLCTEALAAKRRHSOLFSDW 360
 DB 301 TPNFVSNNTSVALLSCTCRSGNLADECEMLEGFFSHNPLCTEALAAKRRHSOLFSDW 360
 QY 361 PPTFAVAHAQNNENPAVRPQWPVPSLFSCTPLILLISLM 400
 DB 361 PPTFAVAHAQNNENPAVRPQWPVPSLFSCTPLILLISLM 400
 QY 378 PPTFAVAHAQNNENPAVRPQWPVPSLFSCTPLILLISLM 378
 DB 378 PPTFAVAHAQNNENPAVRPQWPVPSLFSCTPLILLISLM 378

RESULT 7
 W37462
 W37462 standard; Protein; 315 AA.
 21-MAY-1998 (first entry)
 DE Human Ret ligand RetL3 partial sequence.
 KW Ret ligand; RetL; RetL3; receptor; signal transduction; human;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neurone disease; multiple sclerosis;
 KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
 KW cranial nerve injury; spinal cord injury; Down's syndrome;
 KW cerebral palsy; Lyme disease; muscular dystrophy;

EM myasthenia gravis; tumour; therapy.
 OS Homo sapiens.
 PN W09744356-A2
 PD 27-MAY-1997; U07726.
 PR 07-MAY-1997; U07726.
 PR 10-APR-1997; US-017427.
 PR 08-MAY-1996; US-017427.
 PR 07-JUN-1996; US-019300.
 PR 16-JUL-1996; US-021859.
 PA (BIOJ) BIOGEN INC.
 PI Cate RL, Hession C, Santicola-Nadel M;
 MPI: 98-018431/02.
 DR N-PSDB; V00250.
 DR New nucleic acid encoding ret receptor ligands and related proteins
 PT -vectors, transformed cells and antibodies, used for promoting cell
 PT growth and improving survival of injured cells, especially renal or
 PT nerve cells
 PS Claim 2: Page 81-82; 113pp; English.
 This amino acid sequence comprises a human Ret ligand (RetL) RetL3
 partial polypeptide sequence, deduced from a partial clone (see
 V00250) isolated from a human adult heart cDNA library; a
 full-length RetL3 sequence (see W37463) is also claimed, as well
 as rat and human RetL, human RetL2 and mouse RetL3 sequences
 (see W37455-61). RetL ligand is a key component of the Ret
 signalling pathway that specifically interacts with Ret receptor
 protein, triggering Ret dimerisation and/or autophosphorylation of
 the Ret tyrosine kinase domain. Vectors containing RetL3 DNA and
 prokaryotic or eukaryotic host cells transformed or transfected
 with these vectors are claimed, as well as a method for production
 of RetL3, its soluble variants and fusion proteins with a toxin,
 imageable compound or radionuclide. RetL3, optionally when
 expressed from vectors in vivo, is used to promote growth of new
 tissue and survival of damaged tissue, particularly kidney or
 neural tissue. Typical applications are in renal failure,
 nephritis, kidney transplants, toxic or hypoxic injury,
 neurodegeneration, motor neurone disease, multiple sclerosis,
 bacterial, viral or prion infections (e.g. meningitis, myelopathy
 associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
 spinal cord injury, developmental disorders such as Down's syndrome
 and cerebral palsy, or conditions involving the peripheral nervous
 system (Lyme disease, muscular dystrophy and myasthenia gravis).
 CC Fusion proteins are used to deliver toxins etc. to Ret-expressing
 CC cells, especially tumours.
 CC Sequence 315 AA.
 SQ
 Query Match 78.0%; Score 1708; DB 1; Length 315;
 Best Local Similarity 100.0%; Pred. No. 5e-145;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 92 QLRNSSLICGCMCHRRKKNVACLDIYWTYHARSISLGYELDVSPYEDTYSKPKMKMLSK 151
 7 QLRNSSLICGCMCHRRKKNVACLDIYWTYHARSISLGYELDVSPYEDTYSKPKMKMLSK 66
 152 LNNLKPDSDLCTKFAMLCTLNKCDRLKRAYGACSGPHCORHVCRLQLLTFEKAEPH 211
 67 LNNLKPDSDLCTKFAMLCTLNKCDRLKRAYGACSGPHCORHVCRLQLLTFEKAEPH 126
 212 AGLLLCPCAPNDRCGGERRRNTIAPNCALPPVAPNCLERLRCFSDPLCRSLVDFOTR 271
 127 AGLLLCPCAPNDRCGGERRRNTIAPNCALPPVAPNCLERLRCFSDPLCRSLVDFOTR 186
 272 CHPMDILGATCATEOSRCLAYLGLTAMTPNVSNNVTSSVALSCORSGNIOECCEML 331
 187 CHPMDILGATCATEOSRCLAYLGLTAMTPNVSNNVTSSVALSCORSGNIOECCEML 246
 332 EEFESHNPCLTFAIAAKMFFHSOLFSDQPHPTFAVMAHONENPAVPOWPVSLFSCIT 391
 247 EEFESHNPCLTFAIAAKMFFHSOLFSDQPHPTFAVMAHONENPAVPOWPVSLFSCIT 306
 392 PLILLSLW 400
 307 PLILLSLW 315

RESULT 8
 W37461
 ID W37461 standard; Protein; 397 AA.
 AC W37461;
 DT 21-MAY-1998 (first entry)
 DE Mouse Ret ligand RetL3.
 KW Ret ligand; RetL; RetL3; receptor; signal transduction; mouse;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neurone disease; multiple sclerosis;
 KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
 KW cranial nerve injury; spinal cord injury; Down's syndrome;
 KW cerebral palsy; Lyme disease; muscular dystrophy;
 KW myasthenia gravis; tumour; therapy.
 OS Mus musculus.
 PN W09744356-A2.
 PD 27-NOV-1997.
 PR 07-MAY-1997; U07726.
 PR 10-APR-1997; US-017427.
 PR 08-MAY-1996; US-017427.
 PR 07-JUN-1996; US-019300.
 PR 16-JUL-1996; US-021859.
 PA (BIOJ) BIOGEN INC.
 PI Cate RL, Hession C, Santicola-Nadel M;
 MPI: 98-018431/02.
 DR N-PSDB; V00249.
 DR New nucleic acid encoding ret receptor ligands and related proteins
 PT -vectors, transformed cells and antibodies, used for promoting cell
 PT growth and improving survival of injured cells, especially renal or
 PT nerve cells
 PS Claim 2: Page 77-78; 113pp; English.
 This amino acid sequence comprises mouse Ret ligand (RetL) RetL3,
 CC deduced from cDNA clones (see V00249) isolated from an EST
 CC database and by 5'RACE. Rat and human RetL, human RetL2 and RetL3
 CC sequences (see W37457-60 and W37462-63) are also claimed. RetL is
 CC a key component of the Ret signalling pathway that specifically
 CC interacts with Ret receptor protein, triggering Ret dimerisation
 CC and/or autophosphorylation of the Ret tyrosine kinase domain.
 CC Vectors containing RetL3 DNA and prokaryotic or eukaryotic host
 CC cells transformed or transfected with these vectors are claimed, as
 CC well as a method for production of RetL3. Its soluble variants and
 CC fusion proteins with a toxin, imageable compound or radionuclide.
 CC RetL3, optionally when expressed from vectors in vivo, is used to
 CC promote growth of new tissue and survival of damaged tissue,
 CC particularly kidney or neural tissue. Typical applications are in
 CC renal failure, nephritis, kidney transplants, toxic or hypoxic
 CC injury, neurodegeneration, motor neurone disease, multiple sclerosis,
 CC bacterial, viral or prion infections (e.g. meningitis, myelopathy
 CC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
 CC spinal cord injury, developmental disorders such as Down's syndrome
 CC and cerebral palsy, or conditions involving the peripheral nervous
 CC system (Lyme disease, muscular dystrophy and myasthenia gravis).
 CC Fusion proteins are used to deliver toxins etc. to Ret-expressing
 CC cells, especially tumours.
 CC Sequence 397 AA.
 SQ
 Query Match 75.2%; Score 1646.5; DB 1; Length 397;
 Best Local Similarity 77.8%; Pred. No. 2.1e-139;
 Matches 305; Conservative 30; Mismatches 56; Indels 1; Gaps 1;
 9 PLPPVTLMLLLIPSPPLDLAGDPLPTESRLNNSCLQARRCOADPTCSAAVHHLDSCT 68
 7 PRPP-LIMILLIVLSMLPLGAGNSLATENRFVNSCTQARKKCEANPAKAAVYHLSGCT 65
 69 SSIISTPLSEEPSVPADCEAAQOLRNSSLICGCMCHRRKKNVACLDIYWTYHARSISLN 128
 66 SSIISRLPLEESMSADCEAAEQOLRNSSLIDCRCHRRKHQATCDIYWTYHARSISLD 125
 129 YELDVSPYEDTYSKPKMKMLSKLNNLKPDSDLCTKFAMLCTLNKCDRLKRAYGACSG 188

DB 126 YELDVSPYEDYVTSKPKMNLSTLMKLPDSDCLCFAMCTLDKCDRLKAYGECG 185
 QY 189 PHCORHVALCQLLTFFEKAAEPHAGILLPCAPNDRCGGERRRNTIAPCALPVPAPNC 248
 DB 186 IRCORHICLAQLRSFFEKAAESHAGILLPCAPEDAGCGERRRNTIAPCALPVPAPNC 245
 QY 249 LEIRLRCFSPPLCRSLVDTQTHCHPMIDIGTCATGOSRCLRAYLGLIGTAMPNPNVSV 308
 DB 246 LDLSFCRADPLCRSLMDQTHCHPMIDIGTCATGOSRCLRAYLGLIGTAMPNPNVSV 305
 QY 309 NTSVALSCGSGNLQEECEMLEGFFSHNPCLTETATAAMRRHSOLFSDQWHPPTAV 368
 DB 306 NTSVALSCGSGNLQEECEMLEGFFSHNPCLTETATAAMRRHSOLFSDQWHPPTAV 365
 QY 369 AHONENPAPVAPQWVPSLFCSTLPLILLSLW 400
 DB 366 QOONSMPALRLQPLRLPILSFLILLQTLW 397
 RESULT 9
 182
 W84182 standard; Protein: 397 AA.
 AC W84182;
 DT 25-MAR-1999 (first entry)
 DE A GDNFR-alpha-related protein 3 (GRR3).
 KW Rat; glial cell-line derived neurotrophic factor receptor;
 KW GDNFR; glial cell-line-derived neurotrophic factor; GDNF;
 KW neurturin; signal transduction; dopaminergic nerve cell;
 KW Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;
 KW neurological disorder; diabetes; glaucoma; sensory neuron;
 KW retinal ganglion cell degeneration; sensory neuropathy;
 KW retinopathy; gene therapy; GDNFR-related protein 3; GRR3.
 OS Rattus sp.
 PN WO9854213-A2.
 PD 03-DEC-1998.
 PE 27-APR-1998: U08486.
 PR 30-MAY-1997: US-866354.
 PA (AMGE-) AMGEN INC.
 PI Fox GM, Jing S, Wen D;
 DR N-PSDB: 99-080806/07.
 DR N-PSDB: V99331.
 PT New isolated glial cell line-derived neurotrophic factor receptors -
 PT used to develop products for treating e.g. improperly functioning
 PT dopaminergic nerve cells, Parkinson's disease, Alzheimer's disease
 PT or amyotrophic lateral sclerosis.
 PS Clam 51; Fig 17; 318pp; English.
 CC The present sequence represents a rat glial cell-line derived
 CC neurotrophic factor receptor (GDNFR)-related protein 3 (GRR3).
 CC The protein has similar functions to GDNFR. GDNFR proteins are
 CC functionally characterized by the ability to bind glial cell
 CC line-derived neurotrophic factor (GDNF) and/or neurturin specifically,
 CC and to act as part of a molecular complex which mediates or enhances
 CC the signal transduction affects of GDNF and/or neurturin. The proteins
 CC can be used for treating improperly functioning dopaminergic nerve
 CC cells, Parkinson's disease, Alzheimer's disease or amyotrophic lateral
 CC sclerosis. They can also be used for treating neurological disorders
 CC associated with diabetes, glaucoma or other diseases and conditions
 CC involving retinal ganglion cell degeneration, sensory neuropathy caused
 CC by injury to, insults to, or degeneration of, sensory neurons,
 CC pathological conditions, or disease or injury-related retinopathies.
 CC The products can also be used for detection, diagnosis, drug screening
 CC and gene therapy.
 SQ Sequence 397 AA;

Query Match 75.0%; Score 1642.5; DB 1; Length 397;
 Best Local Similarity 77.2%; Pred. No. 4.8e-139;
 Matches 305; Conservative 30; Mismatches 57; Indels 3; Gaps 1;

QY 6 NBRPLPVVLMILLPPSPPLAGDPLPTESRLMSCLARRKQADPTCSAAYHLD 65
 DB 6 SPRPPLVILLVSL--WLPDIGNSLPTENRNVNCTQARKKCANPCKAAYCHLD 62

QY 66 SCTSSISTPLPSEEPVADCLAAOOLRNSLIGCCRRMKNOVACLDIYTVHARS 125
 DB 63 SCPLSLSPPLPSEESATSAACLEAAOOLRNSLIDRCRRMKHOATCDIYTVHARS 122
 QY 126 LSNVELDVSPYEDYVTSKPKMNLSTLMKLPDSDCLCFAMCTLDKCDRLKAYGECG 185
 DB 123 LSNVELDVSPYEDYVTSKPKMNLSTLMKLPDSDCLCFAMCTLDKCDRLKAYGECG 182
 QY 186 CSOPHQRHVALCQLLTFFEKAAEPHAGILLPCAPNDRCGGERRRNTIAPCALPVP 245
 DB 183 CSOPHQRHVALCQLLTFFEKAAEPHAGILLPCAPEDAGCGERRRNTIAPCALPVP 242
 QY 246 PNCLERLRCFSPPLCRSLVDTQTHCHPMIDIGTCATGOSRCLRAYLGLIGTAMPNPNV 305
 DB 243 PNCLERLRCFSPPLCRSLVDTQTHCHPMIDIGTCATGOSRCLRAYLGLIGTAMPNPNV 302
 QY 306 SNVNTVALSCGSGNLQEECEMLEGFFSHNPCLTETATAAMRRHSOLFSDQWHPPT 365
 DB 303 SNVNTVALSCGSGNLQEECEMLEGFFSHNPCLTETATAAMRRHSOLFSDQWHPPT 362
 QY 366 AYMAHONENPAPVAPQWVPSLFCSTLPLILLSLW 400
 DB 363 SYMAOONSMPALRLQPLRLPILSFLILLQTLW 397
 RESULT 10
 W37465
 W37465 standard; Protein: 346 AA.
 AC W37465;
 DT 21-MAY-1998 (first entry)
 DE Mouse Ret ligand retL3 partial sequence.
 KW Ret ligand; RetL; receptor; signal transduction; mouse;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neuron disease; multiple sclerosis;
 KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
 KW cranial nerve injury; spinal cord injury; Down's syndrome;
 KW cerebral palsy; Lyme disease; muscular dystrophy;
 KW myasthenia gravis; tumour; therapy.
 OS Mus musculus.
 PN WO9744356-A2.
 PD 27-NOV-1997.
 PE 07-MAY-1997: U07726.
 PR 10-APR-1997: US-017427.
 PR 08-MAY-1996: US-017427.
 PR 07-JUN-1996: US-019300.
 PR 16-JUL-1996: US-021859.
 PA (BioT) BIOGEN INC.
 PI Cate RL, Hession C, Santicola-Nadel M;
 DR WPI: 98-018431/02.
 DR N-PSDB: V00256.
 PT New nucleic acid encoding ret receptor ligands and related proteins
 PT - vectors, transformed cells and antibodies, used for promoting cell
 PT growth and improving survival of injured cells, especially renal or
 PT nerve cells.
 PS Disclosure: Page 73-74; 113pp; English.
 CC This polypeptide comprises a partial sequence of mouse Ret ligand
 CC RetL3, deduced from EST A050083 cDNA (see V00256). A full-length
 CC mouse RetL3 sequence (see W37461) was also obtained. Rat, mouse
 CC and human RetL3, retL2 and retL3 cDNA sequences (see V00245-51) and
 CC encoded polypeptides (see W37457-63) are claimed and can be used
 CC in methods for promoting cell growth and improving survival of
 CC cells, especially renal or neural cells.
 SQ Sequence 346 AA;

Query Match 66.4%; Score 1455; DB 1; Length 346;
 Best Local Similarity 80.9%; Pred. No. 2.3e-122;
 Matches 267; Conservative 21; Mismatches 42; Indels 0; Gaps 0;

QY 71 ISPLPSEEPSVPADCLAAOOLRNSLIGCCRRMKNOVACLDIYTVHARSAGYE 130
 DB 17 LSRPLPSEESAMSDCLAAOOLRNSLIDRCRRMKHOATCDIYTVHARSAGYE 76

QY 131 LDVSPYEDVTWTKKWKMLSKLNLKLPDSDICLAFMLCTLNDKCDRLKAYGCAESGP 190
 DB 77 LDVSPYEDVTWTKKWKMLSKLNLKLPDSDICLAFMLCTLNDKCDRLKAYGCAESGP 136
 QY 191 CORAVCLRLTFFERKAEPAHOGILLCPAPNDRCGERRRNTIAPCALPPVAPNLE 250
 DB 137 CORHCLALQLEFFERKAEPAHOGILLCPAPNDRCGERRRNTIAPCALPPVAPNLE 196
 QY 251 LRLCFSDPLCRSLVDFOTCHPMIDIGTCATEOSRCLRAVLIGIGTAMTPNPNVNT 310
 DB 197 LRSCGRADPLCRSLVDFOTCHPMIDIGTCATEOSRCLRAVLIGIGTAMTPNPNVNT 256
 QY 311 SVALSCGRSGNLOECCEMLEGFFSHNPCLTEAIAAMRPHSOLFSDMPHPTFAVAH 370
 DB 257 TVALSCGRSGNLOECCEMLEGFFSHNPCLTEAIAAMRPHSOLFSDMPHPTFAVAH 316
 QY 371 QNENPAPRPPWPSLSCTPLILLSLW 400
 DB 317 QNSNPALRLQPRPLPSILPLILLQTLW 346

RESULT 11

W65118
 ID W65118 standard; Protein; 172 AA.
 AC W65118;
 DT 28-SEP-1998 (first entry)
 DE Human GDNF alpha-3 receptor protein fragment.
 KW Glial cell line-derived neurotrophic factor alpha-3 receptor; GDNF;
 KW treatment; neurodegenerative disease; Parkinson's disease; ALS; SMA;
 KW amyotrophic lateral sclerosis; spinal muscular atrophy; nerve; trauma;
 KW Huntington's disease; Alzheimer's disease; diabetic neuropathy; muscle;
 KW muscular dystrophy; diagnostic.
 OS Homo sapiens.
 FH Key
 FT Location/Qualifiers
 FT 1..172 /label= "GDNF alpha-3"
 FT /note= "Partial sequence"
 EP-846764-A2.
 PN 10-JUN-1998.
 PF 20-NOV-1997; 309375.
 PR 09-MAY-1997; GS-009463.
 PR 27-NOV-1996; GB-024677.
 PA (SMIR) SMITHKLINE BEECHAM PLC.
 PI Lawrence GMP;
 DR MPI: 98-299980/27.
 N-PSDB: V35366.
 CC New factor alpha 3 receptor polypeptide and e.g. DNA and agonists -
 used to treat neuro degenerative diseases, muscular diseases and
 nerve and muscle trauma and in diagnostic assays
 PT Claim 29; Fig 6; 22pp; English.
 CC This sequence represents a fragment from a novel glial cell line-derived
 neurotrophic factor alpha-3 receptor (GDNF alpha-3). This protein can be
 used to treat e.g. neurodegenerative diseases (such as Parkinson's
 Disease), amyotrophic lateral sclerosis (ALS), spinal muscular atrophy
 (SMA), Huntington's Disease, Alzheimer's Disease, diabetic neuropathy,
 CC muscular diseases (including the muscular dystrophies) and nerve and
 muscle trauma and in diagnostic assays for such conditions.
 SO Sequence 172 AA.

Query Match 43.1%; Score 944; DB 1; Length 172;
 Best Local Similarity 100.0%; Pred. No. 4.3e-77;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 ERRRNTIAPCALPPVAPNCLERLCLFSDPLCRSLVDFOTCHPMIDIGTCATEOSRC 288
 DB 1 ERRRNTIAPCALPPVAPNCLERLCLFSDPLCRSLVDFOTCHPMIDIGTCATEOSRC 60
 QY 289 LRAYLIGLIGTAMTPNPNVNTSVALSCGRSGNLOECCEMLEGFFSHNPCLTEAIAAR 348
 DB 61 LRAYLIGLIGTAMTPNPNVNTSVALSCGRSGNLOECCEMLEGFFSHNPCLTEAIAAR 120

QY 349 MRFHSQLESDMPHPTFAVAHONENPAVRPPWPSLSCTPLILLSLW 400
 DB 121 MRFHSQLESDMPHPTFAVAHONENPAVRPPWPSLSCTPLILLSLW 172

RESULT 12

W84183
 ID W84183 standard; Protein; 498 AA.
 AC W84183;
 DT 25-MAR-1999 (first entry)
 DE Consensus sequence of rat and human GDNF and GRN proteins.
 KW Glial cell-line derived neurotrophic factor receptor;
 KW GDNF; glial cell line-derived neurotrophic factor; GDNF;
 KW neurotrophin; signal transduction; dopaminergic nerve cell;
 KW Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;
 KW retinal ganglion cell degeneration; glaucoma; sensory neuron;
 KW retinopathy; gene therapy; GDNF-related protein; GRN.
 OS Synthetic.
 OS Rattus sp.
 OS Homo sapiens.
 FH Key
 FT Location/Qualifiers
 FT MISC.difference 1..498 /note= "x-not specified"
 FT W09854213-A2.
 PN 03-DEC-1998.
 PF 27-APR-1998; U08486.
 PR 30-MAY-1997; US-866354.
 PA (AMGE-) AMGEN INC.
 PI Fox GM, Jing S, Wen D;
 DR MPI: 99-080806/07
 PT New isolated glial cell line-derived neurotrophic factor receptors -
 used to develop products for treating e.g. improperly functioning
 PT dopaminergic nerve cells; Parkinson's disease; Alzheimer's disease
 PT or amyotrophic lateral sclerosis
 PS Claim 51; Fig 19; 31pp; English.
 CC The present sequence represents a consensus sequence of rat and
 CC human glial cell-line derived neurotrophic factor receptor (GDNF)
 CC protein and GDNF-related (GRN) proteins. The proteins have similar
 CC functions. GDNF proteins are functionally characterized by the ability
 CC to bind glial cell line-derived neurotrophic factor (GDNF) and/or
 CC neurotrophin specifically, and to act as part of a molecular complex which
 CC mediates or enhances the signal transduction affects of GDNF and/or
 CC neurotrophin. The proteins can be used for treating improperly functioning
 CC dopaminergic nerve cells; Parkinson's disease; Alzheimer's disease or
 CC amyotrophic lateral sclerosis. They can also be used for treating
 CC neurological disorders associated with diabetes, glaucoma or other
 CC diseases and conditions involving retinal ganglion cell degeneration,
 CC sensory neuropathy caused by injury to, insults to, or degeneration of,
 CC sensory neurons, pathological conditions, or disease or injury-related
 CC retinopathies. The products can also be used for detection, diagnosis,
 CC drug screening and gene therapy.
 SO Sequence 498 AA;

Query Match 28.9%; Score 632.5; DB 1; Length 498;
 Best Local Similarity 40.2%; Pred. No. 1.2e-48;
 Matches 151; Conservative 24; Mismatches 166; Indels 35; Gaps 10;

QY 1 MVRPLNRPPLPYVLMILLPLPSPLPLA---GDPPLPESRLMNSCLDARRKCOADPTC 57
 DB 1 MVRPLNRPPLPYVLMILLPLPSPLPLA---GDPPLPESRLMNSCLDARRKCOADPTC 59
 QY 58 SAAVNHLDSCS--SISTPLPS-EEPSVPADCLLEAQAOLRNSSLICMCHRRKKNQVACT 114
 DB 60 SXXYRRLRQCXGXKXNTYLAISGXEXXKXKXAXEXLXKSLYCRCKRGMKEXXCL 119
 QY 115 DIYWTYHRAISLGNLVDVSPYEDVTWTKKWKMLSKL-----NMLRPDSDL 161
 DB 120 XIYWSHXKXLLXGNXLLXKXNXXLXKXNXXLXKXNXXLXKXNXXLXKXNXXL 174
 QY 162 CLKFALCTLNDKCDRLKAYGAC-----SGPHOGRHVCNLQOLTFEKAAPHAOGSL 216

Db	175	CLDAKACNLNDXCKIKLSAIVIXXCCXXXSXKXECNRKCKHRLAQPFDPVYXXHXXGML	234
Qy	217	LCPCAPBNDRCGGERRRNTIAPNCLPRV-ADNCTELRLCESDPLCRSLRVDFQTHC--H	273
Db	235	FCSCXXXDXMACXERRRQCIYXSCSYEXXKERNKCLDLRXKCTFYDLGRSLADFXTHCXXX	294
Qy	274	PMDLIGCATCQSGHCLRAIYGLIGTAMTPNPNVSNVT--SYALSCTRGSGNLOECEML	331
Db	295	XRXVXSCXANNYXXCLNAYXGLIGTMTPTVDSSTXXVYAPCMCRGSGNXXECEEK	354
Qy	332	EGFESHNPCLTEAIAA	347
Db	355	LXFXKXNPKCLNATQA	370

RESULT	1.3
W84298	
ID	W84298 standard; Protein; 489 AA
AC	W84298.

Consensus sequence of GDNFR and GRR2 and GRR3 proteins.
Glia1 cell-line derived neurotrophic factor receptor.
KW GDNFR, glial cell line-derived neurotrophic factor; GDNF;
KW neurotrophin; signal transduction; dopaminergic nerve cell;
KW Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis
KW neurodegenerative disease; diabetes; glaucoma; sensory neuron;
KW retinal ganglion cell degeneration; sensory neuropathy;
KW retinopathy; gene therapy; GDNFR-related protein; GRR2; GRR3.
OS Synaptic.

Query Match	26.9%;	Score 589.5;	DB 1;	Length 489;
Best Local Similarity	38.8%;	Pred. No. 8e-45;		
Matches 134;	Conservative 22;	Mismatches 160;	Indels 29;	Gaps 8

[illegible]

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Db      84  CXXAAEXLXMSLVDCHCRKRGMRKEXXCXLIYWSHXHXLXGXXLXSPXEMPVTR-- 142
QY      146  KMNLSKLT-----NMKLPBBDLCIFPMMLCTLWDCDRCLRKAYGEMC-----S 187
Db      142  ---LSDIRPXXSXKXKXDXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 198
QY      188  GPCHCRHYVCLROLTFPEKAAEPHAGLILLOPCAPNDRGGERRRNTIYVNCALPV-AP 246
Db      199  XERCNRRCRCHALNQFFPDYKVPXHXHYGMILCSCAXXMXACKERRRQJITXSCSTEXXEXP 256
QY      247  NCLLELRCLCFSDPLCRSLVDVOTCHCPMDILGT-C-ATFQSRCLRAYLIGTAMPNF 304
Db      259  NCLDLRSXCRXDMLCRSRRLDFFXFNCRKXPRXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 318
QY      305  VSNVNT--SVALSCTCRGSGNLOECCMLBGFSFHNCLTEATIAA 347
Db      319  VDSXKTXHXVAPMCKCRGSGNXXECCFKFLXXFXPNCLNNAIOA 363

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RESULT 14
W84181
ID W84181 standard; Protein; 460 AA
AC W84181.

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DE A GDNFR- α -related protein 2 (GRR2).
 KW Rat; glial cell-line derived neurotrophic factor; GDNF;
 KW GDNFR; glial cell line-derived neurotrophic factor; GDNF;
 KW neuritin; signal transduction; dopaminergic nerve cell;
 KW Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis
 KW neurologic disorder; diabetes; glaucoma; sensory neuron;
 KW retinal ganglion cell degeneration; sensory neuropathy;
 KW retinopathy; gene therapy; GDNFR-related protein 2; GRR2.
 OS Rattus sp.

CC injury-related retinopathies. The products can also be used for
CC detection, diagnosis, drug screening and gene therapy.
SQ sequence. 460 AA;

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query Match      25.0%; Score 547.5; DB 1    length 460;
Best Local Similarity   36.0%; Pred. No. 4, 2e-81;
Matches 131; Conservative 45; Mismatches 139; Indels 49; Gaps 11;

QY       19 LLTPSPILAAAGDPLPRTSLNMS-----CIAARRKOADPTCAAYHHIDSTC 68
          |::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db        1 KLVFSSHNPDELTLNSAPSSLGSEELHGWPPVDCRAVELTCAASNCSSRRRTLROCL 60

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OM protein - protein search, using sw model

Run on: December 13, 1999, 02:27:09 ; Search time 29.27 Seconds

(without alignments)
298,605 Million cell updates/sec

Title: US-09-272-835-17

Perfect score: 2022

Sequence: 1 MVRPLNRPPLPPVYIMLLLP...PPVPSLFSCTPLILLISLM 369

Scoring table: BLOSUM62

Searched: 188963 seqs, 23686106 residues

abase: A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1996.5	98.7	400	1	W37463 Human Ret ligand R
2	1996.5	98.7	400	1	W65116 Human GDNF alpha-3
3	1996.5	98.7	400	1	W84186 Gllal cell line-de
4	1992.5	98.5	400	1	A GDNFR-alpha-rela
5	1990.5	98.4	378	1	W65117 Human GDNF alpha-3
6	1849.5	91.5	378	1	W84185 Gllal cell line-de
7	1514.5	74.9	315	1	W37462 Human Ret ligand R
8	1459	72.2	397	1	W84182 A GDNFR-alpha-rela
9	1458	72.1	397	1	W37461 Mouse Ret ligand R
10	1266.5	62.6	346	1	W37465 Mouse Ret ligand R
11	944	46.7	172	1	W65118 Human GDNF alpha-3
12	579	28.6	498	1	W84183 Consensus sequence
13	544	26.9	489	1	W84298 A GDNFR-alpha-rela
14	519	25.7	460	1	W84181 Rat neurotulin rece
15	514	25.4	464	1	W71604 Rat neurotulin rece
16	514	25.4	464	1	W71602 Rat neurotulin rece
17	513	25.4	464	1	W81624 Mouse TGF-beta rel
18	513	25.4	464	1	W81625 Mouse mature TGF-b
19	513	25.4	411	1	W37460 Human Ret ligand R
20	509	25.2	464	1	W71601 Human neurotulin re
21	509	25.2	464	1	W71601 Human neurotulin re
22	509	25.2	664	1	W71603 Human neurotulin re
23	509	25.2	664	1	W81622 Human neurotulin re
24	509	25.2	411	1	W81623 Human mature TGF-b
25	509	25.2	464	1	W84188 Gllal cell line-de
26	509	25.2	464	1	W84179 A GDNFR-alpha-rela
27	509	25.2	464	1	W37459 Human GDNFR-beta P
28	488	24.1	460	1	W37459 Human Ret ligand R
29	485.5	24.0	465	1	W35333 Human Ret ligand R
30	485.5	24.0	465	1	W84163 GDNFR-alpha protei
31	485.5	24.0	463	1	W84166 GDNFR-alpha protei
32	485.5	24.0	463	1	W84167 Human GDNFR-alpha
33	485.5	24.0	465	1	W92300 Human GDNFR-alpha
34	484.5	24.0	465	1	W64165 GDNFR-alpha protei
35	483.5	23.9	468	1	W27327 Rat gllal cell der
36	483.5	23.9	468	1	W35334 Rat gllal cell lin
37	483.5	23.9	468	1	W37457 Rat Ret ligand Rel
38	483.5	23.9	468	1	W84166 Gllal cell-line de
39	476.5	23.6	468	1	W84166 Gllal cell-line de
40	407	20.1	360	1	W22298 Rat GDNFR-alpha po
41	403	19.9	331	1	W81627 Mouse TGF-beta rel
42	379.5	18.8	346	1	W37458 Human Ret ligand R
43	336.5	16.6	232	1	W84168 GDNFR-alpha protei

ALIGNMENTS

RESULT	ID	Sequence	Score	Length	DB ID	Description
1	W37463	W37463 standard; Protein: 400 AA.	336.5	16.6	294	1
2	W37463	W37463	45	210	10.4	219
3	W37463	W37463	45	210	10.4	219
4	W37463	W37463	45	210	10.4	219
5	W37463	W37463	45	210	10.4	219
6	W37463	W37463	45	210	10.4	219
7	W37463	W37463	45	210	10.4	219
8	W37463	W37463	45	210	10.4	219
9	W37463	W37463	45	210	10.4	219
10	W37463	W37463	45	210	10.4	219
11	W37463	W37463	45	210	10.4	219
12	W37463	W37463	45	210	10.4	219
13	W37463	W37463	45	210	10.4	219
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15	W37463	W37463	45	210	10.4	219
16	W37463	W37463	45	210	10.4	219
17	W37463	W37463	45	210	10.4	219
18	W37463	W37463	45	210	10.4	219
19	W37463	W37463	45	210	10.4	219
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23	W37463	W37463	45	210	10.4	219
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27	W37463	W37463	45	210	10.4	219
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32	W37463	W37463	45	210	10.4	219
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34	W37463	W37463	45	210	10.4	219
35	W37463	W37463	45	210	10.4	219
36	W37463	W37463	45	210	10.4	219
37	W37463	W37463	45	210	10.4	219
38	W37463	W37463	45	210	10.4	219
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51	W37463	W37463	45	210	10.4	219
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57	W37463	W37463	45	210	10.4	219
58	W37463	W37463	45	210	10.4	219
59	W37463	W37463	45	210	10.4	219
60	W37463	W37463	45	210	10.4	219
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66	W37463	W37463	45	210	10.4	219
67	W37463	W37463	45	210	10.4	219
68	W37463	W37463	45	210	10.4	219
69	W37463	W37463	45	210	10.4	219
70	W37463	W37463	45	210	10.4	219
71	W37463	W37463	45	210	10.4	219
72	W37463	W37463	45	210	10.4	219
73	W37463	W37463	45	210	10.4	219
74	W37463	W37463	45	210	10.4	219
75	W37463	W37463	45	210	10.4	219
76	W37463	W37463	45	210	10.4	219
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87	W37463	W37463	45	210	10.4	219
88	W37463	W37463	45	210	10.4	219
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91	W37463	W37463	45	210	10.4	219
92	W37463	W37463	45	210	10.4	219
93	W37463	W37463	45	210	10.4	219
94	W37463	W37463	45	210	10.4	219
95	W37463	W37463	45	210	10.4	219
96	W37463	W37463	45	210	10.4	219
97	W37463	W37463	45	210	10.4	219
98	W37463	W37463	45	210	10.4	219
99	W37463	W37463	45	210	10.4	219
100	W37463	W37463	45	210	10.4	219

Query Match: 98.7% Score 1996.5; DB 1; Length 400;
Best Local Similarity: 92.2%; Pred. No. 6.9e-15;
Matches 369; Conservative 0; Mismatches 0; Indels 31; Gaps 1;
1 MVRPLNRPPLPPVYIMLLLP...PPVPSLFSCTPLILLISLM 369
1 MVRPLNRPPLPPVYIMLLLP...PPVPSLFSCTPLILLISLM 369

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QY 61 YHLDSCSTSSISTPLPSEEPVSPADCLAEAAQOLRNSSLIGCMCHRRKNQVACDIYWTV 120
DB 61 YHLDSCSTSSISTPLPSEEPVSPADCLAEAAQOLRNSSLIGCMCHRRKNQVACDIYWTV 120
QY 121 HRAARL-----DSDLCKFAAMCTLNDKCDRLRK 149
DB 121 HRAARLGNVELDVSPYEDVTYVSKPMKNLSKLMKLPDSDCLFAMCTLNDKCDRLRK 180
QY 150 AYGCACSGPHQCRHVCLROLITFEKAAEPHAGLLCPCAPNDGCGERRRNTIAPNCA 209
DB 151 AYGCACSGPHQCRHVCLROLITFEKAAEPHAGLLCPCAPNDGCGERRRNTIAPNCA 240
QY 210 LPFVAPNCLERLRCFSDPLCRSLVDVOTCHPMDLIGTCATQOSRLRAYLGLIGTAM 269
DB 241 LPFVAPNCLERLRCFSDPLCRSLVDVOTCHPMDLIGTCATQOSRLRAYLGLIGTAM 300
QY 270 TPNFVSNVNTSVALSCTCRSGNLOECCEMLEGEFFSHNPCLTEAIAAKMRHSQLFSQDW 329
DB 301 TPNFVSNVNTSVALSCTCRSGNLOECCEMLEGEFFSHNPCLTEAIAAKMRHSQLFSQDW 360
QY 330 PPTFAVAHONENPAVRPOWPVSLFSCITPLILLISLW 369
DB 361 PPTFAVAHONENPAVRPOWPVSLFSCITPLILLISLW 400

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RESULT 2

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W65116
ID W65116 standard; Protein; 400 AA.
AC W65116;
DE 28-SEP-1998 (first entry)
KW Human GDNF alpha-3 receptor protein #1.
KW Glial cell line-derived neurotrophic factor alpha-3 receptor; GDNF;
KW treatment; neurodegenerative disease; Parkinson's disease; ALS; SMA;
KW amyotrophic lateral sclerosis; spinal muscular atrophy; nerve; trauma;
KW Huntington's disease; Alzheimer's disease; diabetic neuropathy; muscle;
KW muscular dystrophy; diagnostic.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Protein 1..400
FT /label= GDNF alpha-3
FT /note= "Partial sequence"
PD EP-846764-A2.
PD 10-JUN-1998.
PD 20-NOV-1997; 309375.
PR 09-MAY-1997; GB-009463.
PR 27-NOV-1996; GB-024677.
PA (SMIR) SMITHKLINE BEECHAM PLC.
LA Lawrence GMP.
WP1: 98-299980/27.
DN N-PSDB: V35364.
PT New factor alpha 3 receptor polypeptide and e.g. DNA and agonists -
PT used to treat neuro degenerative diseases, muscular diseases and
PT nerve and muscle trauma and in diagnostic assays
PS Claim 4; Fig 2; 22pp; English.
CC This sequence represents a novel glial cell line-derived neurotrophic
CC factor alpha-3 receptor (GDNF alpha-3). This protein can be used to
CC treat e.g. neurodegenerative diseases (such as Parkinson's disease,
CC amyotrophic lateral sclerosis (ALS), spinal muscular atrophy (SMA),
CC Huntington's disease, Alzheimer's disease, diabetic neuropathy),
CC muscular diseases (including the muscular dystrophies) and nerve and
CC muscle trauma and in diagnostic assays for such conditions.
SQ Sequence 400 AA;

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Query Match 98.7% Score 1996.5; DB 1: Length 400;
 Best Local Similarity 92.2%; Pred. No. 6,9e-165;
 Matches 369; Conservative 0; Mismatches 0; Indels 31; Gaps 1;

QY 1 MYRLNRPPLPVPVIMLLLPSPPLPLAGDPLPTSRMLNSCLARRCQADPTCSAA 60
 DB 1 MYRLNRPPLPVPVIMLLLPSPPLPLAGDPLPTSRMLNSCLARRCQADPTCSAA 60

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QY 61 YHLDSCSTSSISTPLPSEEPVSPADCLAEAAQOLRNSSLIGCMCHRRKNQVACDIYWTV 120
DB 61 YHLDSCSTSSISTPLPSEEPVSPADCLAEAAQOLRNSSLIGCMCHRRKNQVACDIYWTV 120
QY 121 HRAARL-----DSDLCKFAAMCTLNDKCDRLRK 149
DB 121 HRAARLGNVELDVSPYEDVTYVSKPMKNLSKLMKLPDSDCLFAMCTLNDKCDRLRK 180
QY 150 AYGCACSGPHQCRHVCLROLITFEKAAEPHAGLLCPCAPNDGCGERRRNTIAPNCA 209
DB 151 AYGCACSGPHQCRHVCLROLITFEKAAEPHAGLLCPCAPNDGCGERRRNTIAPNCA 240
QY 210 LPFVAPNCLERLRCFSDPLCRSLVDVOTCHPMDLIGTCATQOSRLRAYLGLIGTAM 269
DB 241 LPFVAPNCLERLRCFSDPLCRSLVDVOTCHPMDLIGTCATQOSRLRAYLGLIGTAM 300
QY 270 TPNFVSNVNTSVALSCTCRSGNLOECCEMLEGEFFSHNPCLTEAIAAKMRHSQLFSQDW 329
DB 301 TPNFVSNVNTSVALSCTCRSGNLOECCEMLEGEFFSHNPCLTEAIAAKMRHSQLFSQDW 360
QY 330 PPTFAVAHONENPAVRPOWPVSLFSCITPLILLISLW 369
DB 361 PPTFAVAHONENPAVRPOWPVSLFSCITPLILLISLW 400

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RESULT 3

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W84186
ID W84186 standard; Protein; 400 AA.
AC W84186;
DE 25-MAR-1999 (first entry)
KW Glial cell line-derived neurotrophic factor receptor gamma 2.
KW Glial cell line-derived neurotrophic factor receptor gamma 2;
KW GDNF alpha; glial cell line-derived neurotrophic factor; GDNF;
KW neurodegenerative disease; amyotrophic lateral sclerosis; GDNF-gamma2;
KW Parkinson's disease; schizophrenia; insomnia; tardive dyskinesia;
KW hypertension; pituitary adenomas; hyperprolactinemia; thyroid tumour;
KW renal disorder; kidney failure; gut dysfunction; regeneration;
KW cardiomyocyte; epithelium; hepatocyte.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..31
FT /label= signal_peptide
FT Protein 32..400
FT /label= mature_protein
FT Domain 32..382
FT /note= "extracellular domain"
FT Domain 383..400
FT /note= "transmembrane domain"
PD W09853069-A2.
PD 26-NOV-1998.
PD 20-MAY-1998; U10328.
PD 27-JUN-1997; US-884638.
PR 20-MAY-1997; US-047092.
PA (HUMA-) HUMAN GENOME SCI INC.
PI Gentz RL, Hsu T, Ni J, Ruben SM, Young P;
WP1: 99-070150/06.
DN N-PSDB: V99334.
PT New isolated glial cell derived neurotrophic factor receptors - used
PT to develop products for treating e.g. neurodegenerative disorders,
PT schizophrenia, hypertension, tumours, renal disorders, kidney
PT failure or gut dysfunction
PS Claim 53; Fig 7A-D; 156pp; English.
CC The present sequence represents a glial cell line-derived neurotrophic
CC factor receptor gamma 2 (GDNF-gamma2). GDNF-gamma2 shares high homology
CC with GDNF-alpha, which is capable of complexing with glial cell
CC line-derived neurotrophic factor (GDNF) and mediating cell response to
CC GDNF. The GDNF polypeptides and agonists can be used for treating
CC disorders associated with decreased activity of the respective
CC polypeptides. They can be used for treating neurodegenerative diseases
CC such as amyotrophic lateral sclerosis, Parkinson's disease,
CC schizophrenia, insomnia, tardive dyskinesia, hypertension, pituitary
CC adenomas, hyperprolactinemia, thyroid tumour, renal disorders, kidney
CC failure, gut dysfunction, or for regeneration of cardiomyocytes.

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epithelium or hepatocytes. Antagonists of the polypeptides can be used for treating disorders associated with increased activity of the respective polypeptides. The products can also be used for detection, diagnosis and drug screening.

Query Match 98.7%; Score 1996.5; DB 1; Length 400;
Best Local Similarity 92.2%; Pred. No. 6,9e-165;
Matches 369; Conservative 0; Mismatches 0; Indels 31; Gaps 1;

1 MYRPLNRPRLPPVYMLLLPLPSPLPLAAGDPLPTESRLMNSCLQARRKCOADPTCSAA 60
1 MYRPLNRPRLPPVYMLLLPLPSPLPLAAGDPLPTESRLMNSCLQARRKCOADPTCSAA 60
61 YHHLDSCTSSISTPLPSEPSVPADCLEAAQOLRNSSLIGCMCHRRKNQVACLDIYTV 120
61 YHHLDSCTSSISTPLPSEPSVPADCLEAAQOLRNSSLIGCMCHRRKNQVACLDIYTV 120
121 HRRSL-----DSDLCIKFAMLCITLNDKCDRLRK 149
121 HRRSL-----DSDLCIKFAMLCITLNDKCDRLRK 149
150 AGEACSGPHCQRHVCRLRLITFEKAAEPHAGGLICPCAPNDRCGGERRNTIAPNCA 209
181 AGEACSGPHCQRHVCRLRLITFEKAAEPHAGGLICPCAPNDRCGGERRNTIAPNCA 240
210 LPPVAPNCLRLCFSDPLCRSLVDVFOHCPMDILGTCAEGRSCLRAYIGLIGTAM 269
241 LPPVAPNCLRLCFSDPLCRSLVDVFOHCPMDILGTCAEGRSCLRAYIGLIGTAM 300
270 TPNFVSNVNTSVSLSTCGSGNLOECCMLEGFFSHNCLTEAIAAKRFSOLFSDW 329
301 TPNFVSNVNTSVSLSTCGSGNLOECCMLEGFFSHNCLTEAIAAKRFSOLFSDW 360
330 PPHFAVMAHONENPAVRQPWPVPSLFSCTPLILLISLM 369
361 PPHFAVMAHONENPAVRQPWPVPSLFSCTPLILLISLM 400

RESULT 4
ID W84180
AC W84180;
DE 25-MAR-1999 (first entry)
A GDNFR-alpha-related protein 3 (GRR3).
Human; glial cell line-derived neurotrophic factor receptor;
GDNFR; glial cell line-derived neurotrophic factor; GDNF;
neurturin; signal transduction; dopaminergic nerve cell;
Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;
neurological disorder; diabetes; glaucoma; sensory neuron;
retinal ganglion cell degeneration; sensory neuropathy;
retinopathy; gene therapy; GDNFR-related protein 3; GRR3.
Homo sapiens.
W09654213-A2.
03-DEC-1998.
27-APR-1998; U08486.
30-MAY-1997; US-866354.
(AMGE-) AMGEN INC. PA
Fox GM, Jing S, Wen D;
WPI; 99-080806/07.
N-PSDB: V99329.

New isolated glial cell line-derived neurotrophic factor receptors -
used to develop products for treating e.g. improperly functioning
dopaminergic nerve cells, Parkinson's disease, Alzheimer's disease
or amyotrophic lateral sclerosis
Claim 51; Fig 15; 318p; English.
The present sequence represents a human glial cell line derived
neurotrophic factor receptor (GDNFR)-related protein 3 (GRR3).
The protein has similar functions to GDNFR. GDNFR proteins are
functionally characterised by the ability to bind glial cell
line-derived neurotrophic factor (GDNF) and/or neurturin specifically,
and to act as part of a molecular complex which mediates or enhances

the signal transduction affects of GDNF and/or neurturin. The proteins
can be used for treating improperly functioning dopaminergic nerve
cells, Parkinson's disease, Alzheimer's disease or amyotrophic lateral
sclerosis. They can also be used for treating neurological disorders
associated with diabetes, glaucoma or other diseases and conditions
involving retinal ganglion cell degeneration, sensory neuropathy caused
by injury to, insults to, or degeneration of, sensory neurons.
The products can also be used for detection, diagnosis, drug screening,
and gene therapy.
Sequence 400 AA;

Query Match 98.5%; Score 1992.5; DB 1; Length 400;
Best Local Similarity 92.0%; Pred. No. 1.5e-164;
Matches 368; Conservative 0; Mismatches 1; Indels 31; Gaps 1;

1 MYRPLNRPRLPPVYMLLLPLPSPLPLAAGDPLPTESRLMNSCLQARRKCOADPTCSAA 60
1 MYRPLNRPRLPPVYMLLLPLPSPLPLAAGDPLPTESRLMNSCLQARRKCOADPTCSAA 60
61 YHHLDSCTSSISTPLPSEPSVPADCLEAAQOLRNSSLIGCMCHRRKNQVACLDIYTV 120
61 YHHLDSCTSSISTPLPSEPSVPADCLEAAQOLRNSSLIGCMCHRRKNQVACLDIYTV 120
121 HRRSL-----DSDLCIKFAMLCITLNDKCDRLRK 149
121 HRRSL-----DSDLCIKFAMLCITLNDKCDRLRK 149
150 AGEACSGPHCQRHVCRLRLITFEKAAEPHAGGLICPCAPNDRCGGERRNTIAPNCA 209
181 AGEACSGPHCQRHVCRLRLITFEKAAEPHAGGLICPCAPNDRCGGERRNTIAPNCA 240
210 LPPVAPNCLRLCFSDPLCRSLVDVFOHCPMDILGTCAEGRSCLRAYIGLIGTAM 269
241 LPPVAPNCLRLCFSDPLCRSLVDVFOHCPMDILGTCAEGRSCLRAYIGLIGTAM 300
270 TPNFVSNVNTSVSLSTCGSGNLOECCMLEGFFSHNCLTEAIAAKRFSOLFSDW 329
301 TPNFVSNVNTSVSLSTCGSGNLOECCMLEGFFSHNCLTEAIAAKRFSOLFSDW 360
330 PPHFAVMAHONENPAVRQPWPVPSLFSCTPLILLISLM 369
361 PPHFAVMAHONENPAVRQPWPVPSLFSCTPLILLISLM 400

RESULT 5
ID W65117
AC W65117;
DE 28-SEP-1998 (first entry)
Human GDNF alpha-3 receptor protein #2.
Glial cell line-derived neurotrophic factor alpha-3 receptor; GDNF;
treatment; neurodegenerative disease; Parkinson's disease; ALS; SMA;
amyotrophic lateral sclerosis; spinal muscular atrophy; nerve; trauma;
Huntington's Disease; Alzheimer's Disease; diabetic neuropathy; muscle;
muscular dystrophy; diagnostic.
Homo sapiens.
Key
FH Key
FT Protein
FT Location/Qualifiers
FT 1..400
FT /label= "GDNF alpha-3
FT /note= "partial sequence"

EP-846764-A2.
10-JUN-1998.
20-NOV-1997; 309375.
09-MAY-1997; GB-009463.
27-NOV-1996; GB-024677.
(SMIK) SKITIKLINE BEECHAM PLC.
Lawrence GMP.
WPI; 98-29980/27.
N-PSDB: V35365.
New factor alpha 3 receptor polypeptide and e.g. DNA and agonists -
used to treat neuro degenerative diseases, muscular diseases and

PT nerve and muscle trauma and in diagnostic assays
 PS Claim 13, Fig 4, 22pp, English.
 CC This sequence represents a novel glial cell line-derived neurotrophic
 CC factor alpha-3 receptor (GDNF alpha-3). This protein can be used to
 CC treat e.g. neurodegenerative diseases (such as Parkinson's disease,
 CC amyotrophic lateral sclerosis (ALS), spinal muscular atrophy (SMA),
 CC Huntington's disease, Alzheimer's disease, diabetic neuropathy,
 CC muscular diseases (including the muscular dystrophies) and nerve and
 CC muscle trauma and in diagnostic assays for such conditions.
 SQ Sequence 400 AA;

Query Match 98.4%; Score 1990.5; DB 1; Length 400;
 Best Local Similarity 92.0%; Pred. No. 2,3e-104;
 Matches 368; Conservative 0; Mismatches 1; Indels 31; Gaps 1;

QY 1 MVRPLNRPPLPPVLMMLLLPPSPPLAAGDPLPTESRLNSCLQARRKQADPTCSAA 60
 DB 1 MVRPLNRPPLPPVLMMLLLPPSPPLAAGDPLPTESRLNSCLQARRKQADPTCSAA 60
 61 YHNDSCSTSSISTPLPSEEPSVPADCLAAQOLNNSLIGCMCHRRKKNQVACDIYWTW 120
 DB 61 YHNDSCSTSSISTPLPSEEPSVPADCLAAQOLNNSLIGCMCHRRKKNQVACDIYWTW 120
 QY 121 HRASLSL-----DSDLCKFAMCTLNKCDRLK 149
 DB 121 HRASLSLGYELDVSPEDYTSKPRKMLSKLMLKPSDCLCKFAMCTLNKCDRLK 180
 QY 150 AYGEACSGPHQORHVCRLQLLTFEKAEPHAQGLLPCAPNDROGGERRRNTIAPNCA 209
 DB 181 AYGEACSGPHQORHVCRLQLLTFEKAEPHAQGLLPCAPNDROGGERRRNTIAPNCA 240
 QY 210 LPPVAPNCLERLRCFSDPLCRSLVDFOYHCHPMDILGTCAEQSRCLRAYLGLIGTAM 269
 DB 241 LPPVAPNCLERLRCFSDPLCRSLVDFOYHCHPMDILGTCAEQSRCLRAYLGLIGTAM 300
 QY 270 TPNFVSNNVTVALSCRCRSGNLOEBCEMLEGFSSHPCLTEAIAKMRHSQLSQDM 329
 DB 301 TPNFVSNNVTVALSCRCRSGNLOEBCEMLEGFSSHPCLTEAIAKMRHSQLSQDM 360
 QY 330 PHPTFAVMAHQNENPAVRPQWPVPSLFSCTLPILLLSLW 369
 DB 361 PHPTFAVMAHQNENPAVRPQWPVPSLFSCTLPILLLSLW 400

RESULT 6
 W84185
 ID W84185 standard; Protein; 378 AA.

25-MAR-1999 (first entry)
 De Glial cell line-derived neurotrophic factor receptor gamma 1.
 KW Glial cell line-derived neurotrophic factor receptor gamma 1;
 KW GDNF-alpha; glial cell line-derived neurotrophic factor; GDNF;
 KW neurodegenerative disease; amyotrophic lateral sclerosis; GDNF-gamma;
 KW Parkinson's disease; schizophrenia; insomnia; tardive dyskinesia;
 KW hypertension; pituitary adenomas; hyperprolactinemia; thyroid tumour;
 KW renal disorder; kidney failure; gut dysfunction; regeneration;
 KW cardiomyocyte; epithelium; hepatocyte.
 OS Homo sapiens.
 FH Key
 FT Peptide 1. 31
 FT /label- signal_peptide
 FT 32. 378
 FT Protein
 FT /label- mature_protein
 FT 32. 360
 FT Domain
 FT /note- "extracellular domain"
 FT 361. 378
 FT /note- "transmembrane domain"
 PN WO853069-A2.
 PD 26-NOV-1998.
 PD 20-MAY-1998; U10328.
 PR 27-JUN-1997; US-884638.
 PR 20-MAY-1997; US-047092.

PA (HOMA-) HUMAN GENOME SCI INC.
 PI Gentz R, Hsu T, NI J, Ruben SM, Young P;
 DR MPI; 99-070150/06.
 DR N-PSDB: V99333.
 PT New isolated glial cell derived neurotrophic factor receptors - used
 PT to develop products for treating e.g. neurodegenerative disorders,
 PT schizophrenia, hypertension, tumours, renal disorders, kidney
 PT failure or gut dysfunction
 PS Claim 26; Fig 4A-C; 156pp; English.
 CC The present sequence represents a glial cell line-derived neurotrophic
 CC factor receptor gamma 1 (GDNF-gamma1). GDNF-gamma1 shares high homology
 CC with GDNF-alpha, which is capable of complexing with glial cell
 CC line-derived neurotrophic factor (GDNF) and mediating cell response to
 CC GDNF. The GDNF polypeptides and agonists can be used for treating
 CC disorders associated with decreased activity of the respective
 CC polypeptides. They can be used for treating neurodegenerative diseases
 CC such as amyotrophic lateral sclerosis, Parkinson's disease,
 CC schizophrenia, insomnia, tardive dyskinesia, hypertension, pituitary
 CC adenomas, hyperprolactinemia, thyroid tumour, renal disorders, kidney
 CC failure, gut dysfunction, or for regeneration of cardiomyocytes,
 CC epithelium or hepatocytes. Antagonists of the polypeptides can be used
 CC for treating disorders associated with increased activity of the
 CC respective polypeptides. The products can also be used for detection,
 CC diagnosis and drug screening.
 SQ Sequence 378 AA;

Query Match 91.5%; Score 1849.5; DB 1; Length 378;
 Best Local Similarity 86.8%; Pred. No. 3.2e-152;
 Matches 347; Conservative 0; Mismatches 0; Indels 53; Gaps 2;

QY 1 MVRPLNRPPLPPVLMMLLLPPSPPLAAGDPLPTESRLNSCLQARRKQADPTCSAA 60
 DB 1 MVRPLNRPPLPPVLMMLLLPPSPPLAAGDPLPTESRLNSCLQARRKQADPTCSAA 60
 61 YHNDSCSTSSISTPLPSEEPSVPADCLAAQOLNNSLIGCMCHRRKKNQVACDIYWTW 120
 DB 61 YHNDSCSTSSISTPLPSEEPSVPADCLAAQOLNNSLIGCMCHRRKKNQVACDIYWTW 120
 QY 121 HRASLSL-----DSDLCKFAMCTLNKCDRLK 149
 DB 121 HRASLSLGYELDVSPEDYTSKPRKMLSKLMLKPSDCLCKFAMCTLNKCDRLK 180
 QY 150 AYGEACSGPHQORHVCRLQLLTFEKAEPHAQGLLPCAPNDROGGERRRNTIAPNCA 209
 DB 181 AYGEACSGPHQORHVCRLQLLTFEKAEPHAQGLLPCAPNDROGGERRRNTIAPNCA 240
 QY 210 LPPVAPNCLERLRCFSDPLCRSLVDFOYHCHPMDILGTCAEQSRCLRAYLGLIGTAM 269
 DB 241 LPPVAPNCLERLRCFSDPLCRSLVDFOYHCHPMDILGTCAEQSRCLRAYLGLIGTAM 300
 QY 270 TPNFVSNNVTVALSCRCRSGNLOEBCEMLEGFSSHPCLTEAIAKMRHSQLSQDM 329
 DB 301 TPNFVSNNVTVALSCRCRSGNLOEBCEMLEGFSSHPCLTEAIAKMRHSQLSQDM 360
 QY 330 PHPTFAVMAHQNENPAVRPQWPVPSLFSCTLPILLLSLW 369
 DB 339 PHPTFAVMAHQNENPAVRPQWPVPSLFSCTLPILLLSLW 378

RESULT 7
 W37462
 ID W37462 standard; Protein; 315 AA.
 AC W37462;
 DT 21-MAY-1998 (first entry).
 DE Human Ret ligand Ret3 partial sequence.
 KW Ret ligand; Ret3; receptor; signal transduction; human;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neurone disease; multiple sclerosis;
 KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
 KW cranial nerve injury; spinal cord injury; Down's syndrome;
 KW cerebral palsy; Lyme disease; muscular dystrophy;

DB 303 SKNTVVALGCTCRGSGNLODECEOLEKSFSONPCLEMAIAAKMRHRLFSDWADSTF 362

QY 335 AVAAHONENPAPVROPVPSLFCSTLPILITLILSLM 369

DB 363 SYWQOONSSPALRPLRLPYLSFFILITLILQTLW 397

RESULT 9

W37461

AC W37461 standard; Protein: 397 AA.

DE Mouse Ret ligand RetL3.

KW Ret ligand; RetL3; receptor; signal transduction; mouse;

KW cell growth; renal cell; nerve cell; renal failure; nephritis;

KW kidney transplant; toxic injury; hypoxic injury;

KW neurodegeneration; motor neurone disease; multiple sclerosis;

KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;

KW cranial nerve injury; spinal cord injury; Down's syndrome;

KW cerebral palsy; Lyme disease; muscular dystrophy;

KW myasthenia gravis; tumour; therapy.

OS Mus musculus.

PN W09744356-A2.

PD 27-NOV-1997.

PF 07-MAY-1997; U07726.

PR 10-APR-1997; US-017427.

PR 08-MAY-1996; US-017427.

PR 07-JUN-1996; US-019300.

PR 16-JUL-1996; US-021859.

PA (BIOJ) BIOGEN INC.

PI Cate RL, Hession C, Sanicola-Nadel M;

DR N-PSDB; V00249.

PT New nucleic acid encoding ret receptor ligands and related proteins

PT - vectors, transformed cells and antibodies, used for promoting cell

PT growth and improving survival of injured cells, especially renal or

PT nerve cells

PS Claim 2; Page 77-78; 113pp; English.

CC This amino acid sequence comprises mouse Ret ligand (RetL) RetL3,

CC deduced from cDNA clones (see V00249) isolated from an EST

CC database and by 5'RACE. Rat and human RetL, human RetL2 and RetL3

CC sequences (see W37457-60 and W37462-63) are also claimed. RetL is

CC a key component of the Ret signalling pathway that specifically

CC interacts with Ret receptor protein, triggering Ret dimerisation

CC and/or autophosphorylation of the Ret tyrosine kinase domain.

CC Vectors containing RetL3 DNA and prokaryotic or eukaryotic host

CC cells transformed or transfected with these vectors are claimed, as

CC well as a method for production of RetL3, its soluble variants and

CC fusion proteins with a toxin, imageable compound or radionuclide.

CC RetL3, optionally when expressed from vectors in vivo, is used to

CC promote growth of new tissue and survival of damaged tissue.

CC particularly kidney or neural tissue. Typical applications are in

CC renal failure, nephritis, kidney transplants, toxic or hypoxic

CC injury, neurodegeneration, motor neurone disease, multiple sclerosis,

CC bacterial, viral or prion infections (e.g. meningitis, myelopathy

CC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or

CC spinal cord injury, developmental disorders such as Down's syndrome

CC and cerebral palsy, or conditions involving the peripheral nervous

CC system (Lyme disease, muscular dystrophy and myasthenia gravis).

CC Fusion proteins are used to deliver toxins etc. to Ret-expressing

CC cells, especially tumours.

SC Sequence 397 AA;

Query Match 72.1%; Score 1458; DB 1: Length 397;

Best Local Similarity 70.2%; Pred. No. 2.2e-118;

Matches 275; Conservative 29; Mismatches 56; Indels 32; Gaps 2;

QY 9 PLPPLVLTLLPLPPSPPLAGDPLPESRLNNSCLQARKCAADPSCAAAYHHDSCT 68

DB 7 PRPPLTLMILLVLSLWPLRAGSLSTATENFVNSCTQARKCANPACRAAYHDSCT 65

QY 69 SSIPTLPSESPVADCLLEAAOOLRNSLIGCMCHRRKKNVACLDIYTWYHARSL-- 127

DB 66 SLSLPLPLEBSAMADCLLEAAOOLRNSLIDCRCHRRKKNVACLDIYTWYHARSLGD 125

QY 127 -----DSDCLKFMCLTLDKDCDLRRAYGEACSG 157

DB 126 YELDVSPYEDVTSKPMKMNLSKLNMLKPDSDCLKFMCLTLDKDCDLRRAYGEACSG 185

QY 158 PHCQRNVLRLQTLTFEEAEPHAGLLCPAPDRCCGERRNTIAPNCALPVPAPNC 217

DB 186 IRCORHLCLAQLRSEFEKAASHAGLLCPAPDRCCGERRNTIAPNCALPVPAPNC 245

QY 218 LELRLCFSDPLCRSRRLVDFCHPMDIIGTCATEGSRCLRAYVGLGTMTPEVSNV 277

DB 246 LDRSFCADPLCRSRRLVDFCHPMDIIGTCATEGSRCLRAYVGLGTMTPEVSNV 305

QY 278 NTSVALSCTCRGSGNLODECEOLEKSFSONPCLEMAIAAKMRHRLFSDWADSTF 337

DB 306 NTVVALSCTCRGSGNLODECEOLEKSFSONPCLEMAIAAKMRHRLFSDWADSTF 365

QY 338 AHONENPAPVROPVPSLFCSTLPILITLILSLM 369

DB 366 QOONSSPALRPLRLPYLSFFILITLILQTLW 397

RESULT 10

W37465

AC W37465 standard; Protein: 346 AA.

DE Mouse Ret ligand RetL3 partial sequence.

KW Ret ligand; RetL3; receptor; signal transduction; mouse;

KW cell growth; renal cell; nerve cell; renal failure; nephritis;

KW kidney transplant; toxic injury; hypoxic injury;

KW neurodegeneration; motor neurone disease; multiple sclerosis;

KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;

KW cranial nerve injury; spinal cord injury; Down's syndrome;

KW cerebral palsy; Lyme disease; muscular dystrophy;

KW myasthenia gravis; tumour; therapy.

OS Mus musculus.

PN W09744356-A2.

PD 27-NOV-1997.

PF 07-MAY-1997; U07726.

PR 10-APR-1997; US-017427.

PR 08-MAY-1996; US-017427.

PR 07-JUN-1996; US-019300.

PR 16-JUL-1996; US-021859.

PA (BIOJ) BIOGEN INC.

PI Cate RL, Hession C, Sanicola-Nadel M;

DR N-PSDB; V00256.

PT New nucleic acid encoding ret receptor ligands and related proteins

PT - vectors, transformed cells and antibodies, used for promoting cell

PT growth and improving survival of injured cells, especially renal or

PT nerve cells

PS Disclosure: Page 73-74; 113pp; English.

CC This polypeptide comprises a partial sequence of mouse Ret ligand

CC RetL3, deduced from EST AA050083 cDNA (see V00256). A full-length

CC mouse RetL3 sequence (see W37461) was also obtained. Rat, mouse

CC and human RetL, RetL2 and RetL3 cDNA sequences (see V00245-51) and

CC encoded polypeptides (see W37457-63) are claimed and can be used

CC in methods for promoting cell growth and improving survival of

CC cells, especially renal or neural cells.

SC Sequence 346 AA;

Query Match 62.6%; Score 1266.5; DB 1: Length 346;

Best Local Similarity 71.8%; Pred. No. 6.5e-102;

Matches 237; Conservative 20; Mismatches 42; Indels 31; Gaps 1;

QY 71 ISPTLPSESPVADCLLEAAOOLRNSLIGCMCHRRKKNVACLDIYTWYHARSL---- 127

DB 17 LSRPLPLEBSAMADCLLEAAOOLRNSLIDCRCHRRKKNVACLDIYTWYHARSLDYE 76

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OY 127 -----DSDLCIFAMLCITLNDKCDRLKRAYGACSGPH 159
DB 77 LDVSPEDYVTSKPKWKNLSKMLKPSDLCIFAMLCITLNDKCDRLKRAYGACSGR 136
OY 160 CORHCLGQLLFFKAAEPHAGLLCPAPNDRCGERRRNTIAPNCPAPVAPNCL 219
DB 137 CORHCLGQLLFFKAAEPHAGLLCPAPNDRCGERRRNTIAPNCPAPVAPNCL 196
OY 220 LRLCFSDPLCRSLVDVOTCHPMDILGTCTEORSRCRAVLIGLTMTNPNVSNVT 279
DB 197 LRSCTADPLCRSLMDVOTCHPMDILGTCTEORSRCRAVLIGLTMTNPNVSNVT 256
OY 280 SVASCTCRSGNLOECEMLEGFSHNPCLEATAAKRFSOLFSDMPHPTFAVMAH 339
DB 257 TVALSCRCRSGNLOECEMLEGFSHNPCLEATAAKRFSOLFSDMPHPTFAVMAH 316
OY 340 ONENPAVPOWVPSLFCSTPLILLSLIM 369
DB 317 QNSNPALRLOPRLPILSFIPLILLQTLW 346

RESULT 11
M65118
ID M65118 standard; Protein; 172 AA.
AC M65118;
DE 28-SEP-1998 (first entry)
KW Human GDNF alpha-3 receptor protein fragment.
KW Glial cell line-derived neurotrophic factor alpha-3 receptor; GDNF;
KW treatment; neurodegenerative disease; Parkinson's disease; ALS; SMA;
KW amyotrophic lateral sclerosis; spinal muscular atrophy; nerve; trauma;
KW Huntington's disease; Alzheimer's disease; diabetic neuropathy; muscle;
KW muscular dystrophy; diagnostic.
KW Homo sapiens.
FH Key Location/Qualifiers
FT 1..172
FT /label= GDNF alpha-3
FT /note= "Partial sequence"
EP-846764-A2.
PD 10-JUN-1998.
PR 20-NOV-1997: 309375.
PR 09-MAY-1997: GB-009463.
PR 27-NOV-1996: GB-024677.
PA (SMIR) SMITHKLINE BEECHAM PLC.
PI Lawrence GMP.
DR WPI: 98-299860/27.
N-PSDB: V35366.
New factor alpha 3 receptor polypeptide and e.g. DNA and agonists -
used to treat neuro degenerative diseases, muscular diseases and
PT nerve and muscle trauma and in diagnostic assays
PS Claim 29; Fig 6; 22pp; English.
CC This sequence represents a fragment from a novel glial cell line-derived
CC neurotrophic factor alpha-3 receptor (GDNF alpha-3). This protein can be
CC used to treat e.g. neurodegenerative diseases (such as Parkinson's
CC disease, amyotrophic lateral sclerosis (ALS), spinal muscular atrophy
CC (SMA), Huntington's disease, Alzheimer's disease, diabetic neuropathy),
CC muscular diseases (including the muscular dystrophies) and nerve and
CC muscle trauma and in diagnostic assays for such conditions.
SQ Sequence 172 AA;

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Query Match 46.7%; Score 944; DB 1; Length 172;
 Best Local Similarity 100.0%; Pred. No. 2e-74;
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 198 ERRRNTIAPNCPALPPVAPNCLERLCSFPLCRSLVDVOTCHPMDILGTCTEORSRC 257
DB 1 ERRRNTIAPNCPALPPVAPNCLERLCSFPLCRSLVDVOTCHPMDILGTCTEORSRC 60
OY 258 LRAVLIGLTMTNPNVSNVTVALSCRCRSGNLOECEMLEGFSHNPCLEATAAK 317
DB 61 LRAVLIGLTMTNPNVSNVTVALSCRCRSGNLOECEMLEGFSHNPCLEATAAK 120

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OY 318 MRFHSQLSQDMPHPTFAVMAHONENPAVPOWVPSLFCSTPLILLSLIM 369
DB 121 MRFHSQLSQDMPHPTFAVMAHONENPAVPOWVPSLFCSTPLILLSLIM 172

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RESULT 12
M84183
ID M84183 standard; Protein; 498 AA.
AC M84183;
DE 25-MAR-1999 (first entry)
KW Consensus sequence of rat and human GDNFR and GRR proteins.
KW Glial cell-line derived neurotrophic factor receptor.
KW GDNFR; glial cell line-derived neurotrophic factor; GDNF;
KW neurotrophin; signal transduction; dopaminergic nerve cell;
KW Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;
KW neurological disorder; diabetes; glaucoma; sensory neuron;
KW retinal ganglion cell degeneration; sensory neuropathy;
KW retinopathy; gene therapy; GDNFR-related protein; GRR.
KW Synthetic.
OS Rattus sp.
OS Homo sapiens.
FH Key Location/Qualifiers
FT MISC.difference 1..498
FT /note= "x-not specified"
FN M09854213-A2.
PD 03-DEC-1998.
PR 27-APR-1998: U08486.
PR 30-MAY-1997: US-866354.
PA (AMGE-) AMGEN INC.
PI Fox GM, Jang S, Men D;
DR WPI: 99-080806/07
PT New isolated glial cell line-derived neurotrophic factor receptors -
PT used to develop products for treating e.g. improperly functioning
PT dopaminergic nerve cells, Parkinson's disease, Alzheimer's disease
PT or amyotrophic lateral sclerosis
PS Claim 51; Fig 19; 318pp; English.
CC The present sequence represents a consensus sequence of rat and
CC human glial cell-line derived neurotrophic factor receptor (GDNFR)
CC protein and GDNFR-related (GRR) proteins. The proteins have similar
CC functions. GDNFR proteins are functionally characterised by the ability
CC to bind glial cell line-derived neurotrophic factor (GDNF) and/or
CC neurotrophin specifically, and to act as part of a molecular complex which
CC mediates or enhances the signal transduction affects of GDNF and/or
CC neurotrophin. The proteins can be used for treating improperly functioning
CC dopaminergic nerve cells, Parkinson's disease, Alzheimer's disease or
CC amyotrophic lateral sclerosis. They can also be used for treating
CC neurological disorders associated with diabetes, glaucoma or other
CC diseases and conditions involving retinal ganglion cell degeneration,
CC sensory neuropathy caused by injury to, insults to, or degeneration of,
CC sensory neurons, pathological conditions, or disease or injury-related
CC retinopathies. The products can also be used for detection, diagnosis,
CC drug screening and gene therapy.
SQ Sequence 498 AA;

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Query Match 28.6%; Score 579; DB 1; Length 498;
 Best Local Similarity 38.0%; Pred. No. 2.4e-42;
 Matches 141; Conservative 22; Mismatches 152; Indels 56; Gaps 10;

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OY 1 MYRPLNRPPLPPVLMILLPLPSPPLIAA---GDLPTSRRLMNSCLARRRCCQADPTC 57
DB 1 MYRPLNRPPLPPVLMILLPLPSPPLIAA---GDLPTSRRLMNSCLARRRCCQADPTC 59
OY 58 SAAYVHLDSCTS--SISTPLPS--EESPVPADCLEAAOQLRNSSLIGCMCHRRKKNOVACL 114
DB 60 SXXYRRLRQCAKXKXMTLASGEXKXKXKXKXAXKXKXSLYOCRCRKKKEXXCL 119
OY 115 DIYWTVA-----RARSLD-----SDLCIKRA 135
DB 120 XIYWSKHXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKXKX 179
OY 136 MCLTLDNCKDRLKRAYGAC-----SGPHCRVVCARQLLTFFKAAEPHAGLLCPA 190

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Db 180 KACLNLDXCKLSSAVYXXKXXXXXKXKRNRRRCRRLROFDKVPYXHXGMLTSCSX 239
 QY 191 PNDGCGERRRNTIAPNCALPV-APNCELRLRCLFSDPLCRSLVDFOTHC--HFMIDL 247
 Db 240 XDXKACERRRRTIPSCSYEXXKRPNCIDLRRXCCRDLCRRLDFXTNCCXXRRXXA 299
 QY 248 GTATDSSRLRLAYLIGLTAMTPNFVSNVT--SYALSTCRGSGNLOECEMELEGFS 305
 Db 300 SCXAXNXXCLMAYXGLIGTAMTPNFVDSSTXXXYAPMCCXGSGNXXECEKFLXFPX 359
 QY 306 HNFCLTEAIA 316
 Db 360 XNFCXNAIOA 370

RESULT 13
 W84298
 ID W84298 standard; Protein: 489 AA.
 DT 25-MAR-1999 (first entry)
 AC W84298;
 KW Consensus sequence of GDNFR and GRR2 and GRR3 proteins.
 NM Glial cell-line derived neurotrophic factor receptor;
 KM GDNFR; glial cell line-derived neurotrophic factor; GDNF;
 KM neurturin; signal transduction; dopaminergic nerve cell;
 KM Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;
 KM neurological disorder; diabetes; glaucoma; sensory neuron;
 KM retinal ganglion cell degeneration; sensory neuropathy;
 KM retinopathy; gene therapy; GDNFR-related protein; GRR2; GRR3.
 OS Synthetic.
 FH Key
 FT Misc-difference 1...489
 TN Location/Qualifiers
 PN W09854213-A2.
 PD 03-DEC-1998.
 PE 27-APR-1998: U08486.
 PR 30-MAY-1997: US-866354.
 PA (AMGE-) AMGEN INC.
 PI Fox GM, Jing S, Wen D;
 DR WPI: 99-080806/07.
 PT New isolated glial cell line-derived neurotrophic factor receptors -
 PT used to develop products for treating e.g. improperly functioning
 PT dopaminergic nerve cells, Parkinson's disease, Alzheimer's disease
 PS or amyotrophic lateral sclerosis
 PS Claim 51; Fig 26; 318pp; English.
 CC The present sequence represents a consensus sequence of glial
 CC cell-line derived neurotrophic factor receptor (GDNFR) protein and
 CC GDNFR-related (GRR) proteins GRR2 and GRR3. The proteins have similar
 CC functions. GDNFR proteins are functionally characterized by the ability
 CC to bind glial cell line-derived neurotrophic factor (GDNF) and/or
 CC neurturin specifically, and to act as part of a molecular complex which
 CC mediates or enhances the signal transduction effects of GDNF and/or
 CC neurturin. The proteins can be used for treating improperly functioning
 CC dopaminergic nerve cells, Parkinson's disease, Alzheimer's disease or
 CC amyotrophic lateral sclerosis. They can also be used for treating
 CC neurological disorders associated with diabetes, glaucoma or other
 CC diseases and conditions involving retinal ganglion cell degeneration,
 CC sensory neuropathy caused by injury to, insults to, or degeneration of,
 CC sensory neurons, pathological conditions, or disease or injury-related
 CC retinopathies. The products can also be used for detection, diagnosis,
 CC drug screening and gene therapy.
 SQ Sequence 489 AA;

Query Match 26.98; Score 544; DB 1; Length 489;
 Best Local Similarity 36.88; Pred. No. 2.5e-39;
 Matches 125; Conservative 20; Mismatches 145; Indels 50; Gaps 8;

QY 27 PLAAADPLPESRLMNSCLQARRCOADPTCSAAYHHLDSCS-SISTPLSEEPSVPAD 85
 Db 24 PLXKX 83
 QY 86 CLEAAGOLRNSLIGCMCHRRMKNOVACLDITVTVH-----RARSL 126

Db 84 CXAXEXLXSSLYDORCKRGMKEXKCLXIYWSHXHXLXKXKXLEXPYEXPTSL 143
 QY 127 D-----SDLCFKFAMCTLNDKCDRLKRAYGEAC-----SGPHCO 161
 Db 144 DIFRXXKX 203
 QY 162 RHYCLRLTLTFEKAEPHNOGLLCPAPNDGCGERRRNTIAPNCALPV-APNCEL 220
 Db 204 RKCKRKLALROFDKVPYXHXGMLTSCSXAXNXXCLMAYXGLIGTAMTPNFVDSST 263
 QY 221 RRLCFSDPLCRSLVDFOTHCHPMDILGT-C-ATDQSRCLRAYLIGLTAMTPNFVSNV 278
 Db 264 RSXCRDLCRRLADFTNCKPAXRXYTXCAXNXXCLMAYXGLIGTAMTPNFVDSX 323
 QY 279 T--SYALSTCRGSGNLOECEMELEGFSHNFCLTEAIA 316
 Db 324 TXXYAPMCCXGSGNXXECEKFLXHXNFCXNAIOA 363

RESULT 14
 W84181
 ID W84181 standard; Protein: 460 AA.
 AC W84181;
 DT 25-MAR-1999 (first entry)
 DE A GDNFR-alpha-related protein 2 (GRR2).
 KW Rat; glial cell-line derived neurotrophic factor receptor;
 KM GDNFR; glial cell line-derived neurotrophic factor; GDNF;
 KM neurturin; signal transduction; dopaminergic nerve cell;
 KM Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;
 KM neurological disorder; diabetes; glaucoma; sensory neuron;
 KM retinal ganglion cell degeneration; sensory neuropathy;
 KM retinopathy; gene therapy; GDNFR-related protein 2; GRR2.
 OS Rattus sp.
 FH Key
 FT Misc-difference 1...460
 TN Location/Qualifiers
 PN W09854213-A2.
 PD 03-DEC-1998.
 PE 27-APR-1998: U08486.
 PR 30-MAY-1997: US-866354.
 PA (AMGE-) AMGEN INC.
 PI Fox GM, Jing S, Wen D;
 DR WPI: 99-080806/07.
 PT New isolated glial cell line-derived neurotrophic factor receptors -
 PT used to develop products for treating e.g. improperly functioning
 PT dopaminergic nerve cells, Parkinson's disease, Alzheimer's disease
 PS or amyotrophic lateral sclerosis
 PS Claim 51; Fig 16; 318pp; English.
 CC The present sequence represents a rat glial cell-line derived
 CC neurotrophic factor receptor (GDNFR)-related protein 2 (GRR2).
 CC The protein has similar functions to GDNFR. GDNFR proteins are
 CC functionally characterized by the ability to bind glial cell
 CC line-derived neurotrophic factor (GDNF) and/or neurturin specifically,
 CC and to act as part of a molecular complex which mediates or enhances
 CC the signal transduction effects of GDNF and/or neurturin. However,
 CC neurturin binds GRR2 more effectively than GDNF, while the reverse is
 CC true for GDNFR. The proteins can be used for treating improperly
 CC functioning dopaminergic nerve cells, Parkinson's disease, Alzheimer's
 CC disease or amyotrophic lateral sclerosis. They can also be used for
 CC treating neurological disorders associated with diabetes, glaucoma or
 CC other diseases and conditions involving retinal ganglion cell
 CC degeneration, sensory neuropathy caused by injury to, insults to, or
 CC degeneration of, sensory neurons, pathological conditions, or disease or
 CC injury-related retinopathies. The products can also be used for
 CC detection, diagnosis, drug screening and gene therapy.
 SQ Sequence 460 AA;

Query Match 25.78; Score 519; DB 1; Length 460;
 Best Local Similarity 34.18; Pred. No. 3.3e-37;
 Matches 122; Conservative 41; Mismatches 127; Indels 68; Gaps 9;

QY 19 LLPPSPPLPAAADPLPESRLMNS-----CLQARRCOADPTCSAAYHHLDSC 68
 Db 1 MLYFPSPHPETRLASLASPSLOGSELHGWRPQYDCAVRANELCAASNSCSRYRTLROCL 60


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QY 69 S--SISTPLSEEPSVPADCLEAAQOLNSSLIGCMCHRRKNQVACLDIYTVH-----122
DB 61 AGDRNTMLANKE-----COAALEVLQESPLDYCRCKRGMKELOCIYIYSHLGLTE114
QY 122 -----RARSIDSDLCLEFAMLCITLNDKCDRLR148
DB 115 GEEFYEAPEYPTVSRSLDIFRLASIFSGTGTDPVSTKSNCLDAARACMLNDCKRLR174
QY 149 KAYGEACS-----GPHCOHRYCLROLITFEFEKAEPHNOGLLPCCANDDGCGERRNT203
DB 175 SYSTISCNRELSPEPRCKRCKHAKLROFEDRVSEYTYRMLFSC--QDACAERRROT232
QY 204 IAPNCAL-PPVAPNCLRLRCLFSDPLCRSLVDFOHCHP--MDILGTCAEQSRCLRA260
DB 233 ILPSCSYEDKEKPCNCLDLRSLCRTDHLCRSLADPHANCRASYRTITSCPADYNOACIGS292
QY 261 YLGLIGTAMTPNFVSNNTSVALS--CTCRGSGNLQECCEMLGFFSHNPCLTEAIAA316
DB 293 YAGMIGDMTPNYDSNPTGIYVSPMCNCRSGNMEECEKFLDFTENPCILRNAIQA350

RESULT 15
ID W71604 standard: Protein; 664 AA.
AC W71604;
DE 19-NOV-1998 (first entry)
DE Rat neuturin receptor alpha/Fc sequence (Ifp2a) fusion protein.
KW Human; neuturin receptor alpha; NTNR-alpha; variant; chimeric;
KW fusion protein; immunoadhesion; ret-expressing cell; neurological;
KW renal; haematological disease.
OS Synthetic.
OS Homo sapiens.
OS Rattus sp.
PN MO9836072-A1.
PD 20-AUG-1998.
PE 17-FEB-1998; 003179.
PR 24-OCT-1997; US-957063.
PR 18-FEB-1997; US-802805.
PR 09-JUN-1997; US-871913.
PA (GEMT) GENENTECH INC.
PI Hyues MA, Klein KD, Rosenthal A;
PI WPI: 98-467175/40.
PT New polypeptide(s) based on human neuturin receptor alpha and
PT ret-expressing cells - useful for increasing survival of
PT ret-expressing cells for treating e.g. neurological, renal and
PT haematological diseases
CC Example 3; Page 84-86; 116pp; English.
CC The present sequence represents rat neuturin receptor alpha
CC (NTNR-alpha)/Fc sequence (Ifp2a) fusion protein, from an example of the
CC (NTNR-alpha)/Fc sequence (Ifp2a) fusion protein, from an example of the
CC present invention. NTNR-alpha proteins can be used: (a) to identify
CC molecules that bind specifically to it (potential agonists and
CC antagonists) and to purify such compounds; (b) to modulate response of
CC cells to neuturin (NTN); (c) to increase survival of ret-expressing
CC neurotrophic factor receptor (GDNFR alpha) may be used the same way;
CC (d) to increase the half-life of cognate ligands (especially NTN); (e)
CC diagnostically to determine serum levels of its ligands; and (f) as
CC animal feed additive or molecular weight marker. NTNR-alpha, its genes,
CC (ant)agonists and antisense nucleic acids, are useful in vivo or ex vivo
CC for treating conditions related to abnormal NTN activity or response,
CC particularly neurological (central or enteric), renal or haematopoietic
CC (spleen) diseases or injuries. Ab may be agonists or antagonists for
CC therapeutic use (e.g. as antagonists to treat excessive/unwanted NTNR-
CC alpha expression, e.g. in some tumours), also reagents for immunoassay
CC and affinity purification.
SQ Sequence 664 AA:

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Query Match 25.4%; Score 514; DB 1; Length 664;
 Best Local Similarity 35.3%; Pred. No. 1.4e-36;
 Matches 114; Conservative 38; Mismatches 113; Indels 58; Gaps 8;

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QY 44 CLOARRCOADPTCSAAYHHLDST--SISTPLSEEPSVPADCLEAAQOLNSSLIGC101
DB 40 CVRAMEICAEESNCSNRRRLROCLAGDRNTMLANE-----COAALEVLQESPLYDC93
QY 102 MCHRRKNQVACLDIYTVH-----RA123
DB 94 RCRGMKRELQCIYIYSHLGLTEGEEFYEAPEYPTVSRSLDIFRLASIFSGTGDPA153
QY 124 RSLSDLCLEFAMLCITLNDKCDRLRKAYGEACS-----GPHCOHRYCLROLITFEFEKAEL178
DB 154 VSTRSNHCLDAARACMLNDCKRLRSSYISICNNEISPTERCKRCKHAKLROFEDRVPS213
QY 179 PHAGLLCPCAPNDRCGERRNTIAPNCAL-PPVAPNCLRLRCLFSDPLCRSLVDFOHCHP237
DB 214 EYTYRMLFSC--QDACAERRROTILPSCSYEDKEKPCNCLDLRSLCRTDHLCRSLADP271
QY 238 QTHCHP--MDILGTCAEQSRCLRAYLGLTAMTPNFVSNNTSVALS--CTCRGSGNL293
DB 272 HANCRASYRTITSCPADYNOACIGS YAGMIGDMTPNYDSNPTGIYVSPMCNCRSGNMEECEKFLDFTENPCILRNAIQA354
QY 294 QEECEMLEGFFSHNPCLTEAIAA316
DB 332 EEECEKFLDFTENPCILRNAIQA354

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Search completed: December 13, 1999, 02:27:10
 Job time: 440 sec

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 13, 1999, 02:19:33 ; Search time 33.26 Seconds
(Without alignments)
736.683 Million cell updates/sec

Title: US-09-272-835-15

Perfect score: 1 MVRPLNRPRLPPVIMLLIL.....PWVPSLSCCTLPILLISIM 400

Sequence: 1 MVRPLNRPRLPPVIMLLIL.....PWVPSLSCCTLPILLISIM 400

Scoring table: BLOSUM62

Searched: 199794 seqs, 61255205 residues

abase :
1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2187	99.9	400	4	060609	060609 homo sapien
2	1646.5	75.2	397	11	035118	035118 mus musculu
3	1643.5	75.0	397	11	035243	035243 mus musculu
4	1641.5	75.0	397	11	035325	035325 mus musculu
5	542.5	24.8	464	11	035977	035977 rattus norv
6	540.5	24.7	464	4	015316	015316 homo sapien
7	540.5	24.7	464	4	015328	015328 homo sapien
8	517.5	23.6	460	4	015507	015507 homo sapien
9	516	23.6	465	4	043912	043912 homo sapien
10	514.5	23.5	463	11	035252	035252 mus musculu
11	513	23.4	468	11	035246	035246 mus musculu
12	512.5	23.4	463	13	035748	035748 rattus norv
13	497.5	22.7	431	13	035312	035312 gallus gall
14	418.5	19.1	358	11	092283	092283 mus musculu
15	408	18.6	330	11	092282	092282 mus musculu
16	147	6.7	2704	5	097458	097458 diosophila
17	133.5	6.1	2653	5	025253	025253 lucilia cup
18	123.5	5.6	2195	5	020462	020462 caenorhabd
19	122.5	5.6	3857	11	088840	088840 mus musculu
20	120	5.5	1964	11	035442	035442 mus musculu
21	115	5.3	850	4	095804	095804 homo sapien
22	115	5.3	5376	11	088799	088799 mus musculu
23	114	5.2	1999	4	099940	099940 homo sapien
24	114	5.2	2003	4	000306	000306 homo sapien
25	114	5.2	9954	4	099466	099466 homo sapien
26	114	5.2	1034	11	035888	035888 rattus norv
27	113.5	5.2	2026	4	000468	000468 homo sapien
28	109.5	5.0	949	5	P90956	P90956 caenorhabd
29	109	5.0	580	4	000634	000634 homo sapien

30	108.5	5.0	4545	11	061291	061291 mus musculu
31	108	4.9	989	4	094909	094909 homo sapien
32	107	4.9	1698	5	094438	094438 chironomus
33	107	4.9	1792	13	057484	057484 gallus gall
34	106	4.8	473	5	025464	025464 mytilus gall
35	104	4.7	2352	5	061240	061240 halocynthia
36	104	4.7	1203	11	006008	006008 mus musculu
37	104	4.7	2470	10	035516	035516 mus musculu
38	103	4.7	2150	5	044131	044131 caenorhabd
39	102.5	4.7	1581	13	073809	073809 fugu rubrip
40	101.5	4.6	1681	5	077244	077244 chlorohydra
41	101	4.6	1077	3	074853	074853 schizosach
42	100	4.6	2408	4	092566	092566 homo sapien
43	100	4.6	1513	5	017970	017970 caenorhabd
44	100	4.6	1254	13	09YH02	09YH02 brachydantio
45	98.5	4.5	468	13	09Y195	09Y195 rana rugosa

ALIGNMENTS

RESULT 1
ID 060609 PRELIMINARY; PRT; 400 AA.
AC 060609;
DT 01-ANG-1998 (TREMBLrel. 07, Created)
DT 01-ANG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-ANG-1998 (TREMBLrel. 07, Last annotation update)
DE GDNF FAMILY RECEPTOR ALPHA 3.
GN GFR3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA BALCH R.H., GORODINSKY A., GOLDEN J.P., TANSEY M.G., KECK C.L.,
RA FOPESCU N.C., JOHNSON E.M., JR., MILLBRAND J.,
RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(1998). 5/98
DR EMBL: AF051767; AAC24355.1; --
SQ SEQUENCE 400 AA; 44538 MW; 6DFB5381 CRC32;

Query Match	99.9%	Score 2187;	DB 4;	Length 400;
Best Local Similarity	99.8%	Pred. No. 3.6e-214;		
Matches 399;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
QY 1	MVRPLNRPRLPPVIMLLILPPSPPLAAGDPLPTESHLMNSCLQARRKCOADPTCSAA	60		
DB 1	MVRPLNRPRLPPVIMLLILPPSPPLAAGDPLPTESHLMNSCLQARRKCOADPTCSAA	60		
QY 61	YHLDSCISSTPLPSEPSVPADCLERAQGLRNSSLIGCMCHRRMKNOVACLDIYTV	120		
DB 61	YHLDSCISSTPLPSEPSVPADCLERAQGLRNSSLIGCMCHRRMKNOVACLDIYTV	120		
QY 121	HRASLGNTLVSPEDVYTSKPMKMLSKIMLKPPSDCLTKAMCTLDKCDRLRK	180		
DB 121	HRASLGNTLVSPEDVYTSKPMKMLSKIMLKPPSDCLTKAMCTLDKCDRLRK	180		
QY 181	AYGAGSGPHCRHVCRLRLTFEFAAEPHAQGLLCPGAPNDGCGERRRNTAPNCA	240		
DB 181	AYGAGSGPHCRHVCRLRLTFEFAAEPHAQGLLCPGAPNDGCGERRRNTAPNCA	240		
QY 241	LEPVAPNCELERLCFSPDLCLRSRLVDFTOCHPMDILGTCTEDSRLRAYLIGITAM	300		
DB 241	LEPVAPNCELERLCFSPDLCLRSRLVDFTOCHPMDILGTCTEDSRLRAYLIGITAM	300		
QY 301	TENFVSNTVTSVALSCTCGSGNLQECGMEGFSSHNPCLTEATAARKRFHSOLFSDW	360		
DB 301	TENFVSNTVTSVALSCTCGSGNLQECGMEGFSSHNPCLTEATAARKRFHSOLFSDW	360		
QY 361	PAPTFAYAHQENPFAVRQPVVPSLFCSTLPILLISIM 400			
DB 361	PAPTFAYAHQENPFAVRQPVVPSLFCSTLPILLISIM 400			

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RESULT 2
ID 035118 PRELIMINARY; PRT: 397 AA.
AC 035118:
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE GLIAL CELL LINE DERIVED NEUROTROPHIC FACTOR FAMILY RECEPTOR ALPHA 3
(GFRALPHA-3).
GN GFR3 OR GFRALPHA-3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL6; TISSUE-HEART;
RX MEDLINE; 98205811.
RA NOMOTO S., ITO S., YANG L.-X., KIUCHI K.;
Molecular cloning and expression analysis of GFR alpha-3, a novel
cDNA related to GDNF alpha and NTR alpha.
Biochem. Biophys. Res. Commun. 244:849-853(1998).
RN [1]
RP SEQUENCE FROM N.A.
RA BALOH R.H., GORODINSKY A., GOLDEN J.P., TANSEY M.G., KECK C.L.,
POBESCU N.C., JOHNSON E.M. JR., MILBRANT J.;
Proc. Natl. Acad. Sci. U.S.A. 0:0-0(1998).
DR EMBL; AB008833; BAA23562.1; -
DR EMBL; AF051766; AAC24354.1; -
DR MGI; MGI:1201403; GFR3.
SQ SEQUENCE 397 AA; 44307 MW; A80EDD24 CRC32;

Query Match 75.28; Score 1646.5; DB 11; Length 397;
Best Local Similarity 77.88; Pred. No. 2,7e-159;
Matches 305; Conservative 30; Mismatches 56; Indels 1; Gaps 1;

OY 9 PLPPVTLMLLLPSPPLAAGDPLPTESRLNSCLQARRKCOADPTCSAAVYHLLDSC 68
DB 7 PRPP-LMLTLVLVSLMPLDAGNSLATERFVNSCTQARRKCEANPACKAAVOHLSCT 65
OY 69 SSISTPLPSEEPSPADCLAEAOQLRNSSLIGCMCHRMKQVACLDIYTVHARSIGN 128
DB 66 SLSPLPLPESASADCLAEAOQLRNSSLIDCRHRMKAQACLDIYTVHARSIGN 125
OY 129 YELVSPEDTVTSKPMKNTSKLMLKPPSDLCLEFAMCTLDKCDRLKAYGEACSG 188
DB 126 YELVSPEDTVTSKPMKNTSKLMLKPPSDLCLEFAMCTLDKCDRLKAYGEACSG 185
OY 189 PHGRHVCRLRLTFEFAKAPHAQGLLCCACAPNDKCGERRRNTIAPNCALPVPAPNC 248
DB 186 IRCGRHVCRLRLTFEFAKAPHAQGLLCCACAPNDKCGERRRNTIAPNCALPVPAPNC 245
OY 249 LELRLCFSPDLCSRLVDFOTCHPMIDLGTCATEOSRCLRAVLGLIGTAMPNFSY 308
DB 246 LDRSFCRADPLCSRLMDROTCHPMIDLGTCATEOSRCLRAVLGLIGTAMPNFSY 305
OY 309 NTSVALSCTCGSGNLOECECEMLGFFSHNPLCTEALIAKMFHSOLFSDWPHPTFAVM 368
DB 306 NTVVALSCTCGSGNLOECECEMLGFFSHNPLCTEALIAKMFHSOLFSDWPHPTFAVM 365
OY 369 AHONENPAVROPWPVPSLFCSTPLILLISLM 400
DB 366 QOONSFPALRLQPRPLISLIPILLIQLTM 397.

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DT 01-JUN-1998 (Tremblrel. 06, Last annotation update)
DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR FAMILY RECEPTOR ALPHA-3.
GN GFR3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RA WIDENFALK J., TOMAC A., LINDQVIST E., HOFER B., OLSON L.;
Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA NAVEITHAN P., BAUDERT C., MIKAELS O., SHEN L., WESTPHAL H.,
ERNFORS P.;
Proc. Natl. Acad. Sci. U.S.A. 0:0-0(1997).
DR EMBL; AF041842; AAC23558.1; -
DR EMBL; AF036163; AAC24468.1; -
SQ SEQUENCE 397 AA; 44302 MW; F77607CF CRC32;

Query Match 75.08; Score 1643.5; DB 11; Length 397;
Best Local Similarity 77.04; Pred. No. 5,5e-159;
Matches 305; Conservative 31; Mismatches 59; Indels 1; Gaps 1;

OY 5 LNRPPLPVTLMLLLPSPPLAAGDPLPTESRLNSCLQARRKCOADPTCSAAVYHLL 64
DB 3 LSLPRLPP-LMLTLVLVSLMPLDAGNSLATERFVNSCTQARRKCEANPACKAAVOH 61
OY 65 DSCSSISTPLPSEEPSPADCLAEAOQLRNSSLIGCMCHRMKQVACLDIYTVHARS 124
DB 62 GSCSSISRLPLPESASADCLAEAOQLRNSSLIDCRHRMKAQACLDIYTVHARS 121
OY 125 SLGNYELVSPEDTVTSKPMKNTSKLMLKPPSDLCLEFAMCTLDKCDRLKAYGE 184
DB 122 SLGNYELVSPEDTVTSKPMKNTSKLMLKPPSDLCLEFAMCTLDKCDRLKAYGE 181
OY 185 ACGSPHGRHVCRLRLTFEFAKAPHAQGLLCCACAPNDKCGERRRNTIAPNCALP 244
DB 182 ACGSPHGRHVCRLRLTFEFAKAPHAQGLLCCACAPNDKCGERRRNTIAPNCALP 241
OY 245 APNCLELRCLFSPDLCSRLVDFOTCHPMIDLGTCATEOSRCLRAVLGLIGTAMP 304
DB 242 TPNCLELRCLFSPDLCSRLVDFOTCHPMIDLGTCATEOSRCLRAVLGLIGTAMP 301
OY 305 VSNVNTSVALSCTCGSGNLOECECEMLGFFSHNPLCTEALIAKMFHSOLFSDWPHPT 364
DB 302 ISKNTVNTSVALSCTCGSGNLOECECEMLGFFSHNPLCTEALIAKMFHSOLFSDWPHPT 361
OY 365 FAYMAHONENPAVROPWPVPSLFCSTPLILLISLM 400
DB 362 FSYVOOONSFPALRLQPRPLISLIPILLIQLTM 397

RESULT 4
ID 035325 PRELIMINARY; PRT: 397 AA.
AC 035325:
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-AUG-1998 (Tremblrel. 07, Last annotation update)
DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR FAMILY RECEPTOR ALPHA-3.
GN GFR3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RA TROPP M., RAYNOSCHER C., IBANEZ C.F.;
Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF020305; AAB70931.1; -
SQ SEQUENCE 397 AA; 44333 MW; F0C0C841 CRC32;

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Query Match 75.0%; Score 1641.5; DB 11; Length 397;
 Best Local Similarity 77.6%; Pred. No. 8.8e-159;
 Matches 304; Conservative 30; Mismatches 57; Indels 1; Gaps 1;

DB 9 PLPPVATMLLLPLPSPLPLAAGDPLPESRLMNSCLARRKCOADPTCSAAVHHLDSC 68
 7 PRPP-LLMILLVLLSLMPLGAGNSLATEFRVNSCTGARRKCEANPACKAYOHGSGT 65
 69 SSIPTPLSEPSVADCLLEAAQOLNSSLICGCHRRKKNVACLDIYTVHARSIGL 128
 66 SLSLSPLELESAMADCLLEAAQOLNSSLIDRCHRRKHQATCLDIYTVHARSIGL 125
 129 YELDVSPEDVTSKPMKNSKLNKLPDSDCLKFMALCTLNKCORLBRAYGEACSG 188
 126 YELDVSPEDVTSKPMKNSKLNKLPDSDCLKFMALCTLNKCORLBRAYGEACSG 185
 189 PHCRHVCRLQLTEFFEKAAEPHAGLLCPAPNDRCGERRRTIAPNCALPVAENC 248
 186 IRCORHLCAGLRSFFEKAAESHAGLLCPCPEDACGERRRTIAPNCALPVAENC 245
 249 LELRCLCESDPLCSRLVDFTCHGPHDILGTGATESRCLRAYIGLIGTANTPVSANV 308
 246 LELRCLCESDPLCSRLVDFTCHGPHDILGTGATESRCLRAYIGLIGTANTPVSANV 305
 309 NTVALSCCTGSGNLOECCMLGEGFSHNPCLTEAIAKKRPHSOLSPHPTFAVM 368
 306 NTVALSCCTGSGNLOECCMLGEGFSHNPCLTEAIAKKRPHSOLSPHPTFAVM 365
 369 AHONENPAVRPQVPSPLFSCPLPILLSLM 400
 366 QOONSNPALRLQPLPLFSLPILLSLM 397

RESULT 5
 035977 PRELIMINARY; PRT; 464 AA.

ID 035977; PRELIMINARY; PRT; 464 AA.
 AC 035977;
 DT 01-JAN-1998 (TEMBREL. 05, Last sequence update)
 DT 01-JAN-1998 (TEMBREL. 05, Last sequence update)
 DT 01-AUG-1998 (TEMBREL. 11, Last annotation update)
 DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR-BETA (GDNF RECEPTOR-BETA).
 GN GDNF-BETA OR RETL.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 [1]
 SEQUENCE FROM N.A.
 TRUMP M., RAYNOSCHER C., IBANEZ C.F.;
 Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 [2]
 SEQUENCE FROM N.A.
 TISSUE-BRAIN/KIDNEY;
 MEDLINE; 97322356.
 RA SANICOLA M., HESSON C.A., WORLEY D.S., CARMILLO P., EHRENFELDS C., WALUS L., ROBINSON S., JAWORSKI G., WEI H., TIZARD R., WHITTY A., PEPINSKY R.B., CAPE R.L.;
 Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 [4]
 SEQUENCE OF 1-444 FROM N.A.
 TISSUE-HIPOCAMPUS;
 SUVANTO P., WATTIOVARA K., LINDAHL M., MOSHAYAROV M., ARDUE U., HORELLI-KUITUNEN N., AIRAKSINEN M.S., PALOTIE A., SAARA M.;
 Cloning, mRNA distribution and chromosomal localization of the gene

RT for glial cell line-derived receptor beta, a homolog to
 RT GDNF-alpha;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF005226; AAB62247.1;
 DR EMBL; U97143; AAC53301.1;
 DR EMBL; AF003825; AAD09310.1;
 KW Receptor.
 SO SEQUENCE 464 AA; 51668 MW; B1A2BD11 CRC32;

Query Match 24.8%; Score 542.5; DB 11; Length 464;
 Best Local Similarity 37.4%; Pred. No. 4.1e-47;
 Matches 123; Conservative 42; Mismatches 125; Indels 39; Gaps 10;

DB 44 CLOARRKCOADPTCSAAVHHLDSCS--SISTPLSEPSVADCLLEAAQOLNSSLICG 101
 40 CVRANELCAESNCSRRITRQCLAGDRNTMLANKE-----COALEVLQSSPLYDC 93
 102 MCHRRKNQVACLDIYTVHARSIGLVDSPEDVTSKPMKNSKLNKLPDSDCLKFMALCTLNKCORLBRAYGEACSG 156
 94 RCKRGMKELQCLQIYMSHGLGEGEPEYASPYE-PVTSR-----LSDFRLASIFSG 147
 156 -----KPSDCLKFMALCTLNKCORLBRAYGEACSG-----GPHCRHVCRLQLTEFF 203
 148 TGIDPAVSTSNHCLDAKACNTLNDCKRLSSYISICNREISPTERCNRRKCHKALROF 207
 204 FEKAEPHAGLLCPAPNDRCGERRRTIAPNCAL-PPVAPNCLELRCLFSPDLR 262
 208 FDRPSETYTRMLFCSC--ODQCAERKROTILPSCSYEDKERNCLDLSLRTHLCR 265
 263 SRLVDFTCHGPHDILGTGATESRCLRAYIGLIGTANTPVSANVNTVALS--CTC 318
 266 SRLADFNANCRAVYRTISCPADNYQACLSYAGMIGFDMTPVYNSNPFIYVSPRCNC 325
 319 RGSNLOECCMLGEGFSHNPCLTEAIAA 347
 326 RGSNMECEKEFLRDTENPCLNMAIOA 354

RESULT 6
 015316 PRELIMINARY; PRT; 464 AA.

ID 015316; PRELIMINARY; PRT; 464 AA.
 AC 015316;
 DT 01-JAN-1998 (TEMBREL. 05, Last sequence update)
 DT 01-JAN-1998 (TEMBREL. 05, Last sequence update)
 DT 01-AUG-1998 (TEMBREL. 07, Last annotation update)
 DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR BETA.
 GN GDNF-BETA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 [1]
 SEQUENCE FROM N.A.
 TISSUE-FETAL BRAIN;
 RA WATTIOVARA K., SUVANTO P., HORELLI-KUITUNEN N., LINDAHL M., MOSHAYAROV M., AIRAKSINEN M.S., PALOTIE A., SANICOLA M., SUVANTO P., WATTIOVARA K., LINDAHL M., MOSHAYAROV M., ARDUE U., HORELLI-KUITUNEN N., AIRAKSINEN M.S., PALOTIE A., SAARA M.;
 Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U93703; AAB61922.1;
 SO SEQUENCE 464 AA; 51530 MW; DE80D543 CRC32;

Query Match 24.7%; Score 540.5; DB 4; Length 464;
 Best Local Similarity 36.5%; Pred. No. 6.6e-47;
 Matches 120; Conservative 47; Mismatches 123; Indels 39; Gaps 10;

DB 44 CLOARRKCOADPTCSAAVHHLDSCS--SISTPLSEPSVADCLLEAAQOLNSSLICG 101
 40 CVRANELCAESNCSRRITRQCLAGDRNTMLANKE-----COALEVLQSSPLYDC 93
 102 MCHRRKNQVACLDIYTVHARSIGLVDSPEDVTSKPMKNSKLNKLPDSDCLKFMALCTLNKCORLBRAYGEACSG 153
 94 RCKRGMKELQCLQIYMSHGLGEGEPEYASPYE-PVTSR-----LSDFRLASIFSG 147

OY 153 ----NNLKPDSDLCRAMELCTINDKCDRLKRAYGACS-----GPHCRHVCRLROLTE 203
 DB 148 TGADPVYSAKSNCLDAKAKCNLNDCKKLRSSYISICNEISPTERRKCHKALRPF 207
 OY 204 FKAAPAEHAGLLCPAPDRGCGERRRTIAPNCAL-PPVAPNCLERLRLCFSPDLR 262
 DB 208 FDRVPESEYTRMLFCSC--ODOACAERRRQTIIPSCSYEDKEKPNCLDLRGVCRTHLDR 265
 OY 263 SRLVDFOTCHP--MDLIGTCATEGSCRLRAYLGLTAMTPFVSNVTSVALS--CTC 318
 DB 266 SRLADPHANCRASYQVYTSPPANTOACIGASIGMIGFDMTPNYVDSPTGIYVSPWCSC 325
 OY 319 RGSNGNLOECCMLEGFEFSHNPCLTEAIAA 347
 DB 326 RGSNGNEECERFLRDPTEPCLRNAIQA 354
 RESULT 7
 ID 015328 PRELIMINARY; PRT; 464 AA.
 015328;
 01-JAN-1998 (TREMblrel. 05, Created)
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
 DE 01-NOV-1998 (TREMblrel. 08, Last annotation update)
 GN RET LIGAND 2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LIVER;
 RX MEDLINE; 97322356.
 RA SANICOLA M., HESSION C.A., WORLEY D.S., CARMILLO P., EHRENFELS C.,
 RA WALUS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
 RA PEPINSKY R.B., CATE R.L.;
 RT "Glial cell line-derived neurotrophic factor-dependent RET activation
 can be mediated by two different cell-surface accessory proteins.";
 RT Proc. Natl. Acad. Sci. U.S.A. 94:6238-6243(1997).
 DR EMBL; U97145; AAC51647.1;
 SO SEQUENCE 464 AA; 51543 MW; 288A8BD8 CRC32;

Query Match 24.7%; Score 540.5; DB 4; Length 464;
 Best Local Similarity 36.5%; Pred. No. 6.6e-47;
 Matches 120; Conservative 47; Mismatches 123; Indels 39; Gaps 10;

OY 44 CLOARRKCOADPTCSAAYHHLDSTG--SISTPLPSEEPVADCLLEAAOQLRNSLIGC 101
 DB 102 MCHRRKNNOVADLIYWTYHARRASGNYLDVSPEDYTSKPMKANKSL----- 153
 DB 94 RKRGRKAKLQCLQITWSTHGLTBEFEYEASPYE-PTTSR-----ISDIFRLASIFSG 147
 OY 153 ----NNLKPDSDLCRAMELCTINDKCDRLKRAYGACS-----GPHCRHVCRLROLTE 203
 DB 148 TGADPVYSAKSNCLDAKAKCNLNDCKKLRSSYISICNEISPTERRKCHKALRPF 207
 OY 204 FKAAPAEHAGLLCPAPDRGCGERRRTIAPNCAL-PPVAPNCLERLRLCFSPDLR 262
 DB 208 FDRVPESEYTRMLFCSC--ODOACAERRRQTIIPSCSYEDKEKPNCLDLRGVCRTHLDR 265
 OY 263 SRLVDFOTCHP--MDLIGTCATEGSCRLRAYLGLTAMTPFVSNVTSVALS--CTC 318
 DB 266 SRLADPHANCRASYQVYTSPPANTOACIGASIGMIGFDMTPNYVDSPTGIYVSPWCSC 325
 OY 319 RGSNGNLOECCMLEGFEFSHNPCLTEAIAA 347
 DB 326 RGSNGNEECERFLRDPTEPCLRNAIQA 354

RESULT 8

015507
 ID 015507 PRELIMINARY; PRT; 460 AA.
 AC 015507;
 DT 01-JAN-1998 (TREMblrel. 05, Created)
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
 DE 01-NOV-1998 (TREMblrel. 08, Last annotation update)
 GN RET LIGAND 1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-KIDNEY;
 RX MEDLINE; 97322356.
 RA SANICOLA M., HESSION C.A., WORLEY D.S., CARMILLO P., EHRENFELS C.,
 RA WALUS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
 RA PEPINSKY R.B., CATE R.L.;
 RT "Glial cell line-derived neurotrophic factor-dependent RET activation
 can be mediated by two different cell-surface accessory proteins.";
 RT Proc. Natl. Acad. Sci. U.S.A. 94:6238-6243(1997).
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-SUBSTANTIA NIGRA;
 RX HISHIKI T., KONDOH K., ICHIMITA S., NIMURA Y., SEKI N., OZAKI T.,
 RA SAKITAWA S., TAKAHASHI H., OHNOMA N., TANBE M., FUJIMURA S.,
 RA NAKAGAWA A.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U97144; AAC51646.1;
 DR EMBL; U95847; AAB71811.1;
 SO SEQUENCE 460 AA; 50838 MW; 022FECA CRC32;

Query Match 23.6%; Score 517.5; DB 4; Length 460;
 Best Local Similarity 36.2%; Pred. No. 1.4e-44;
 Matches 129; Conservative 45; Mismatches 135; Indels 47; Gaps 12;

OY 17 LLLLPSPDLAA---GDLPTESRLMNSCLQARRKCOADPTCSAAYHHLDSTG--- 70
 DB 6 LYFALPLDLILLSAEVSGDRL-----DCVNASDQCLKEGOSTFTRLRQCVAKKE 57
 OY 70 ----SISTPLPSEEPVADCLLEAAOQLRNSLIGCMCHRRKNNOVADLIYWTYHARRSL 126
 DB 58 TNFSLASGLEAKD-----ECRSAMEALOKSLYNCRCRKGKKKKNCLRIYMSWOSIQ- 112
 OY 127 GNYELDVSPEDYTSKPMKANKSLNKLK-----PSDLCRAMELCTINDKCDRL 178
 DB 112 GNOLLEDSPEY-----PVNRLSDIFRYVPFISVENHLPKNNCLDAKAKCNLDIDCKRY 165
 OY 179 KRAYGAC----GPHCRHVCRLROLTEFEKAAPAEHAGLLCPAPDRGCGERRRT 234
 DB 166 RSAVITPCTTSVSNVNDVNRKCHKALRQFEDKVPKAKSYGLFCSC--RDIACTERRROT 223
 OY 235 IAPNCALPP-VAPNCLERLRLCFSPDLRSLVDFOTCHPMD-ILGTCAEO-SRLCRA 291
 DB 224 IVPVCSYEEERKPNCLMLQDSCKTNYICRSLADFTNCPDEBSVSSCKENYADCLLA 283
 OY 292 YLGLIGTAMTPNFVSNVTSVALSCTCRGSGNLOECCMLEGFEFSHNPCLTEAIAA 347
 DB 284 YSGILGVTMPTNYIDSSLSVAPWCDCSNGNDLEBCLKLFNFKNFTCLKNAIQA 339

RESULT 9
 ID 043912 PRELIMINARY; PRT; 465 AA.
 AC 043912;
 AC 043912;

RC STRAIN-C57; TISSUE-LIVER;
RA DEY B.K., WONG Y.W., TOO H.P.;
RL Neuroreport 9:0-0(0001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-C57; TISSUE-LIVER;
RA DEY B.K., WONG Y.W., TOO H.P.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF014117; AAB86599.1;
SQ SEQUENCE 468 AA; 51751 MW; AFDCE6A1 CRC32;

Query Match 23.4%; Score 513; DB 11; Length 468;
Best Local Similarity 36.1%; Pred. No. 4.1e-44;
Matches 130; Conservative 46; Mismatches 134; Indels 50; Gaps 13;

QY 14 VLMLLLPPSPPLAAGDPLPTESRLNSCLQARRKQADPTCSAAYHHLDSTCS--- 70
DB 9 VLPLDLMLSA--EVSGGDRL-----DCVAKSDQCLKEQSCSTYRTLRQCVACKET 58
DU 70 --SISTPLPEEPSPVADCLAAAOQLNSSLIGCMCHRRKNQVACIDIVYTHARASLG 127
DU 59 NFSLISGLEAKD-----ECRSAMEALOKSLYNCRCRKGKKKCNCLRIYMSYQSLQ-G 112
QY 128 NYELDVSPYEDVTYSKPMKNLSKLNLRK-DSDL-----CLKFAMLCITLNDK 174
DB 113 NDLEDSPE-----PVNSRLSDIFRAVPFISDVFOQVEHISKNNCLDAAKACINDDT 166
QY 175 CDRLKRAYGEAC---SGPHQORHVCLROLTFEKAEPHAOGILLPCAPNDROGGER 230
DB 167 CKRYRSAYITPCTTSMNSNENCNKCKHAKALROFFDKYPAHSGMLFCSC--RDVACTER 224
QY 231 RRNTIAPNCALPP-VAPNCLERLRCLFSDPLCRSLVDFOFHCHPMD-ILGTCTAEO-SR 287
DB 225 RROTIYVPCSYERERERNCINLQDCKTNYICRSRLADFPTNCQPSRSVSNCKENYAD 284
QY 288 CLRAYGLISTAMTPNVSVMNTSVALSCTCRSGSNLQECCEMLEGFFSHNPLCTEALIA 347
DB 285 CLAYSGLISTVMTPTNTIDSSLSVAPWCDCSSNSGNDLECLAFNFKDNTCLKNAIOA 344

RESULT 12

035748 PRELIMINARY; PRT; 463 AA.

AC 035748; 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JAN-1998 (TREMBLrel. 05, Last annotation update)
DL GDNFR-ALPHA/TRNR1-DELTA PROTEIN.
U Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HANNOVER;
RA ZHONG J., ANNETS M., HEIMANN R.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL, AJ002072; CA05171.1;
SQ SEQUENCE 463 AA; 51032 MW; 93277F91 CRC32;

Query Match 23.4%; Score 512.5; DB 11; Length 463;
Best Local Similarity 36.0%; Pred. No. 4.6e-44;
Matches 128; Conservative 44; Mismatches 137; Indels 47; Gaps 12;

QY 17 LLLPLPPSPPLA--GDPLTESRLNNSCLQARRKQADPTCSAAYHHLDSTCS--- 70
DB 6 LVFALPLDLMLSAEVSQDRL-----DCVAKSDQCLKEQSCSTYRTLRQCVACKET 57
QY 70 ---SISTPLPEEPSPVADCLAAAOQLNSSLIGCMCHRRKNQVACIDIVYTHARASL 126
DB 58 TNFSLISGLEAKD-----ECRSAMEALOKSLYNCRCRKGKKKCNCLRIYMSYQSLQ- 112

QY 127 GNYELDVSPYEDVTYSKPMKNLSKLNLRK-----DSDLCLKFAMLCITLNDKDR 178
DB 112 GNDLEDSPE-----PVNSRLSDIFRAVPFISVHEHISGNCLDAAKACINDDTCKKY 165
QY 179 RRAYGEAC---SGPHQORHVCLROLTFEKAEPHAOGILLPCAPNDROGGERRRNT 234
DB 166 RRAYITPCTTSMNSNENCNKCKHAKALROFFDKYPAHSGMLFCSC--RDVACTERROT 223
QY 235 IAFNCALPP-VAPNCLERLRCLFSDPLCRSLVDFOFHCHPMD-ILGTCTAEO-SRCLRA 291
DB 224 IYVPCSYERERERNCINLQDCKTNYICRSRLADFPTNCQPSRSVSNCKENYADCL 283
QY 292 YLGLISTAMTPNVSVMNTSVALSCTCRSGSNLQECCEMLEGFFSHNPLCTEALIA 347
DB 284 YSLIGITVMTPTNTIDSSLSVAPWCDCSSNSGNDLECLAFNFKDNTCLKNAIOA 339

RESULT 13

093512 PRELIMINARY; PRT; 431 AA.

AC 093512; 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DE GFR RECEPTOR ALPHA 4 PRECURSOR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 98313402.
RA THOMPSON J., DOXAKIS E., PINON L.G., STRACHAN P., BUT-BELLO A.,
RA WYATT S., BUCHMAN V.L., DAVIES A.M.,
RT "GFRalpha-4, a new GDNF family receptor."
RL Mol. Cell. Neurosci. 11:117-126(1998).
DR EMBL, AF045162; AAC36464.1;
KW signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 431 AA; 47964 MW; 7AE1F0B0 CRC32;

Query Match 22.7%; Score 497.5; DB 13; Length 431;
Best Local Similarity 34.8%; Pred. No. 1.4e-42;
Matches 111; Conservative 37; Mismatches 148; Indels 23; Gaps 8;

QY 44 CLARRKQADPTCSAAYHHLDSTCSISTPLPSEPSVPADCLAAAOQLNSSLIGCMC 103
DB 26 CLAGESECTNDPICSCKFTLRQCLIA--GNGANKLGPDAKNGCRSTYVALSSQLYGCCK 83
QY 104 HRRMNOVACIDIVYTHARASLGNYELDVSPYEDVTYSKPMKNLSKLNLRKPSD--- 161
DB 84 KRGMKEKHCHLSVYSIHHTLMEGNVLSESPYEPFING---FDYVRLASTAGSENEY 139
QY 151 ---CLKFAMLCITLNDKDRKRAYGEAC---SGPHQORHVCLROLTFEKAEPHA 211
DB 140 TQVNNCLAAKACNDVEMCGRLRTYVSFCIRRLARADTCRCKHAKLRKFFDVPPPEY 199
QY 212 AAGLLCPCAPNDROGGERRRNTIAPNCAL-PPVAPNCLERLRCLFSDPLCRSLVDPT 270
DB 200 THELFPCPC--EDFACARROTIVPACSYESKEKPCNLADPSCRENYVCRSRYAEQF 257
QY 271 HCHP-NDLIGTCATEO-SRCLRAYIGLGTAMTPNVSVMNTSVALSCTCRSGSNLQEC 328
DB 258 NCQPSLQTSACRNDSTYACLAATYTGILGSPITPYIDNSTSIAPWCCTNAGSNGRQEC 317
QY 329 EMLGFFSHNPLCTEALIA 347
DB 318 ESFLHFTDNVCIONAIOA 336

RESULT 14

0922A3

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 12, 1999, 19:58:52 ; Search time 27.76 seconds
(without alignments)
679.673 Million cell updates/sec

Title: US-09-272-835-15

Sequence: 1 MVRPLNPPLPPVVMILL.....PWVPSLFSCTPLILLISLM 400

Scoring table: BLOSUM62

Searched: 142080 seqs, 47169319 residues

Database:

PIR62:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1646.5	75.2	397	2 JE0082	GPI-linked receptor
2	147	6.7	2703	1 A24420	notch protein - fr
3	133.5	6.1	3084	1 MMMSA	laminin alpha-1 ch
4	124	5.7	1700	2 S08167	Balbiani ring 3 pr
5	123.5	5.6	3002	2 A47221	fibrillin 1 precu
6	123.5	5.6	2871	2 A55567	fibrillin 1 - Dovi
7	120	5.5	1964	2 T09059	notch - mouse
8	117.5	5.4	2704	2 S09118	G surface protein
9	116	5.3	3635	2 T10053	laminin alpha 5 ch
10	115	5.3	2531	2 A46019	Notch-1 protein -
11	114.5	5.2	2871	2 A55624	fibrillin-1 precu
12	114	5.2	2531	2 S5188	notch protein homo
13	114	5.2	1034	2 JCS598	mucin - rat
14	112.5	5.1	4543	1 A53102	alpha-2-macroglobu
15	112.5	5.1	2535	1 A40043	notch protein homo
16	111.5	5.1	1609	1 MMH082	laminin gamma-1 ch
17	111.5	5.1	1106	2 T13938	gene shuttle craft
18	110	5.0	4544	1 S02392	alpha-2-macroglobu
19	110	5.0	2321	2 S78549	notch3 protein - h
20	109	5.0	2139	2 A35672	crumbs protein - f
21	108.5	5.0	4545	1 S25111	G surface protein
22	108	4.9	2718	2 A23475	alpha-2-macroglobu
23	106	4.8	2918	2 A54105	G surface protein
24	105	4.8	473	2 A56175	fibrillin-2 precu
25	105	4.8	1607	1 MMMS2	adhesive plaque pr
26	105	4.8	1959	1 AGRT	laminin gamma-1 ch
27	105	4.8	553	2 S45281	coagulation factor
28	105	4.8	3075	2 S14458	laminin alpha-1 ch
29	105	4.8	2907	2 A57278	fibrillin-2 precu
30	104	4.7	1639	2 MMFB2	laminin gamma-1 ch
31	104	4.7	593	1 GYHR	granulin precursor
32	104	4.7	2471	2 A49128	cell-fate determin
33	104	4.7	1203	2 A49175	Notch B protein -
34	103.5	4.7	384	2 S25771	Notch 3 protein - mou
35	102.5	4.7	2318	2 S45306	probable vitelloge
36	100.5	4.6	1984	2 T13171	acroglycin - guine
37	99.5	4.5	591	2 S55632	deoxyribonuclease
38	98	4.5	509	1 S55632	hypothetical prote
39	98	4.5	1808	2 T15099	

40 97.5 4.5 540 2 BA7417 Insulin receptor-T
41 97.5 4.5 996 2 JE0237 apolipoprotein E r
42 97.5 4.5 589 2 C38128 epithelin/granulin
43 97 4.4 833 2 S19087 gene delta protein
44 97 4.4 754 2 S17063 fibrillin (clone M
45 96.5 4.4 4753 1 A47437 LDL-receptor-relat

ALIGNMENTS

RESULT 1
JE0082
GPI-linked receptor precursor - mouse
N:Alternate names: GfRalpha-3
C:Species: Mus musculus (house mouse)
C:Date: 21-May-1998 #sequence_revision 29-May-1998 #text_change 17-Mar-1999
C:Accession: JE0082; MUID:98205811
R:Nomoto, S.; Ito, S.; Yang, L.X.; Kirsch, K.
B:Biochem Biophys. Res. Commun. 244, 849-853, 1998
A:Title: Molecular cloning and expression analysis of GfRalpha-3, a novel CDNA related
A:Reference number: JE0082; MUID:98205811
A:Accession: JE0082
A:Molecule type: mRNA
A:Residues: 1-397 <NOM>
A:Cross-references: DDB:AB008833; NID:G2627159; PID:G2627160
C:Comment: This protein plays a distinct role in cell survival and differentiation.
C:Keywords: glycoprotein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:380-397/Region: hydrophobic
F:92,145,306/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 75.2%; Score 1646.5; DB 2; Length 397;
Best Local Similarity 77.8%; Pred. No. 5.4e-123;
Matches 305; Conservative 30; Mismatches 56; Indels 1; Gaps 1;

QY	9	PLPPVVMILLPLPPPLPLAGDPLPTESRLNLSCLQARRKCOADPTCSAAYHHNDSC	68
DB	7	PRPP-LMILLVLVSLWPLPLAGNSLATENFVNSCTQARRKCANPACRAVOHIGSCT	65
QY	69	SSISPLPSEEPSPADCLPAAOOLRNSSLICGCHRMNOVACLDITYTVHARSGLN	128
DB	66	SSLRPLPPLPESASACLEAEOLRNSSLIDCRHRMHQATCTDITYTVHARSGLD	135
QY	129	YELDVSPYEDTVYSKPKMNLSTKMLKPPSDCLKPFAMCTLNDCKDRKAYGACSG	188
DB	126	YELDVSPYEDTVYSKPKMNLSTKMLKPPSDCLKPFAMCTLNDCKDRKAYGACSG	185
QY	189	PHCRHYCLKQLTFPEKAAEPHAGILLPCAPAPNDRCGERRRNTIAPNCALPYAPNC	248
DB	186	IRCRHCLQALRSEFEKAAESHAGILLPCAPAPNDRCGERRRNTIAPNCALPYAPNC	245
QY	249	LELRALFSDPLCRSLRYDQTHCHPMDITGATCDSRCLRAYLGIGTAMPNVSAYN	308
DB	246	LDLRSFRADPLCRSLRYDQTHCHPMDITGATCDSRCLRAYLGIGTAMPNVSAYN	305
QY	309	NTSYALCTCRGSGNLQEECEMLEGFFSHNPLCTEAIAAKMRHSOLFSDMHPFFAYN	368
DB	306	NTSYALCTCRGSGNLQEECEMLEGFFSHNPLCTEAIAAKMRHSOLFSDMHPFFAYN	365
QY	369	AHQENPAPVPPQWVPSLFSCTPLILLISLM 400	
DB	366	QOQNSNPALRQPLPLPSIPLILLISLM 397	

RESULT 2
A24420
notch protein - fruit fly (Drosophila melanogaster)
N:Alternate names: neurogenic repetitive locus protein
C:Species: Drosophila melanogaster
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A24420; A24768; S09358; A05267;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 13, 1999, 02:41:35 ; Search time 20.22 seconds

(without alignments)
575.390 Million cell updates/sec

Title: US-09-272-835-15
Perfect score: 2190

Sequence: 1 MVRPLNRPRLPVVLMILL.....PWPSLSFSCPLILILSLM 400

Scoring table: BLOSUM62

Searched: 80000 seqs, 29085965 residues

Abase: SwissProt_38:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	568	25.9	1 NRTN_CHICK	013157 gallus gall
2	544.5	24.9	2 NRTN_MOUSE	008642 mus musculu
3	540.5	24.7	1 NRTN_HUMAN	000451 homo sapien
4	536.5	24.5	1 GDNF_CHICK	013156 gallus gall
5	533	23.4	1 GDNF_MOUSE	097785 mus musculu
6	511	23.1	1 GDNF_RAT	062997 rattus norv
7	505.5	23.1	1 GDNF_HUMAN	056159 homo sapien
8	147	6.7	1 NRTN_MOUSE	P07207 drosophila
9	133.5	6.1	1 NRTN_MOUSE	P19137 mus musculu
10	124	5.7	1 BARK_CHICK	003336 chironomus
11	123.5	5.6	1 FBNI_BOVIN	098133 bos taurus
12	123.5	5.6	1 FBNI_HUMAN	035555 homo sapien
13	120	5.5	1 NTC4_MOUSE	P31695 mus musculu
14	117.5	5.4	1 G168_PAPPR	P17053 paramecium
15	116	5.3	1 LMA5_MOUSE	061001 mus musculu
16	115	5.3	1 NTC1_MOUSE	001705 mus musculu
17	114.5	5.2	1 NTC1_RAT	007008 rattus norv
18	114	5.2	1 NTC1_MOUSE	061554 mus musculu
19	112.5	5.1	1 LRP1_CHICK	098157 gallus gall
20	112.5	5.1	1 NTC1_HUMAN	P46531 homo sapien
21	111.5	5.1	1 LMG1_HUMAN	P11047 homo sapien
22	111.5	5.1	1 LMG1_HUMAN	P40798 drosophila
23	110	5.0	1 LRP1_HUMAN	007954 homo sapien
24	108	4.9	1 CRB_DROME	P10040 drosophila
25	109	4.9	1 G156_PAPPR	P13837 paramecium
26	106	4.8	1 FBNI_HUMAN	P33556 homo sapien
27	105	4.8	1 FBNI_HUMAN	P25304 rattus norv
28	105	4.8	1 FBNI_HUMAN	P98140 bos taurus
29	105	4.8	1 FBNI_MOUSE	061555 mus musculu
30	105	4.8	1 FBNI_HUMAN	P25591 homo sapien
31	105	4.8	1 LMG1_MOUSE	P02468 mus musculu
32	104	4.7	1 LMG1_MOUSE	P28799 homo sapien
33	103.5	4.7	1 GRN_HUMAN	001721 mus musculu
34	102.5	4.7	1 GRN_MOUSE	061982 mus musculu
35	100.5	4.6	1 YL_DROME	P98163 drosophila
36	100	4.6	1 LMG1_DROME	P15151 drosophila
37	99.5	4.5	1 GRN_MOUSE	P28797 caria porce
38	98	4.5	1 LRP2_HUMAN	P98164 homo sapien
39	97	4.4	1 LRP2_HUMAN	021313 caenorhabd1
40	96.5	4.4	1 LRP2_HUMAN	004833 caenorhabd1
41	96	4.4	1 LRP2_HUMAN	P14585 caenorhabd1
42	95.5	4.4	1 LRP2_HUMAN	061483 mus musculu
43	95.5	4.4	1 LRP2_HUMAN	P98155 homo sapien

ALIGNMENTS

RESULT	ID	Query Match Length	Score	DB	Description
1	1 NRTN_CHICK	25.9	568	1	013157 gallus gall
2	2 NRTN_MOUSE	24.9	544.5	2	008642 mus musculu
3	1 NRTN_HUMAN	24.7	540.5	1	000451 homo sapien
4	1 GDNF_CHICK	24.5	536.5	1	013156 gallus gall
5	1 GDNF_MOUSE	23.4	533	1	097785 mus musculu
6	1 GDNF_RAT	23.1	511	1	062997 rattus norv
7	1 GDNF_HUMAN	23.1	505.5	1	056159 homo sapien
8	1 NRTN_MOUSE	6.7	147	1	P07207 drosophila
9	1 NRTN_MOUSE	6.1	133.5	1	P19137 mus musculu
10	1 BARK_CHICK	5.7	124	1	003336 chironomus
11	1 FBNI_BOVIN	5.6	123.5	1	098133 bos taurus
12	1 FBNI_HUMAN	5.6	123.5	1	035555 homo sapien
13	1 NTC4_MOUSE	5.5	120	1	P31695 mus musculu
14	1 G168_PAPPR	5.4	117.5	1	P17053 paramecium
15	1 LMA5_MOUSE	5.3	116	1	061001 mus musculu
16	1 NTC1_MOUSE	5.3	115	1	001705 mus musculu
17	1 NTC1_RAT	5.2	114.5	1	007008 rattus norv
18	1 NTC1_MOUSE	5.2	114	1	061554 mus musculu
19	1 LRP1_CHICK	5.1	112.5	1	098157 gallus gall
20	1 NTC1_HUMAN	5.1	112.5	1	P46531 homo sapien
21	1 LMG1_HUMAN	5.1	111.5	1	P11047 homo sapien
22	1 LMG1_HUMAN	5.1	111.5	1	P40798 drosophila
23	1 LRP1_HUMAN	5.0	110	1	007954 homo sapien
24	1 CRB_DROME	4.9	108	1	P10040 drosophila
25	1 G156_PAPPR	4.9	109	1	P13837 paramecium
26	1 FBNI_HUMAN	4.8	106	1	P33556 homo sapien
27	1 FBNI_HUMAN	4.8	105	1	P25304 rattus norv
28	1 FBNI_HUMAN	4.8	105	1	P98140 bos taurus
29	1 FBNI_MOUSE	4.8	105	1	061555 mus musculu
30	1 FBNI_HUMAN	4.8	105	1	P25591 homo sapien
31	1 LMG1_MOUSE	4.8	105	1	P02468 mus musculu
32	1 LMG1_MOUSE	4.7	104	1	P28799 homo sapien
33	1 GRN_HUMAN	4.7	103.5	1	001721 mus musculu
34	1 GRN_MOUSE	4.7	102.5	1	061982 mus musculu
35	1 YL_DROME	4.6	100.5	1	P98163 drosophila
36	1 LMG1_DROME	4.6	100	1	P15151 drosophila
37	1 GRN_MOUSE	4.5	99.5	1	P28797 caria porce
38	1 LRP2_HUMAN	4.5	98	1	P98164 homo sapien
39	1 LRP2_HUMAN	4.4	97	1	021313 caenorhabd1
40	1 LRP2_HUMAN	4.4	96.5	1	004833 caenorhabd1
41	1 LRP2_HUMAN	4.4	96	1	P14585 caenorhabd1
42	1 LRP2_HUMAN	4.4	95.5	1	061483 mus musculu
43	1 LRP2_HUMAN	4.4	95.5	1	P98155 homo sapien

RESULT	ID	Query Match Length	Score	DB	Description
1	1 NRTN_CHICK	25.9	568	1	013157 gallus gall
2	2 NRTN_MOUSE	24.9	544.5	2	008642 mus musculu
3	1 NRTN_HUMAN	24.7	540.5	1	000451 homo sapien
4	1 GDNF_CHICK	24.5	536.5	1	013156 gallus gall
5	1 GDNF_MOUSE	23.4	533	1	097785 mus musculu
6	1 GDNF_RAT	23.1	511	1	062997 rattus norv
7	1 GDNF_HUMAN	23.1	505.5	1	056159 homo sapien
8	1 NRTN_MOUSE	6.7	147	1	P07207 drosophila
9	1 NRTN_MOUSE	6.1	133.5	1	P19137 mus musculu
10	1 BARK_CHICK	5.7	124	1	003336 chironomus
11	1 FBNI_BOVIN	5.6	123.5	1	098133 bos taurus
12	1 FBNI_HUMAN	5.6	123.5	1	035555 homo sapien
13	1 NTC4_MOUSE	5.5	120	1	P31695 mus musculu
14	1 G168_PAPPR	5.4	117.5	1	P17053 paramecium
15	1 LMA5_MOUSE	5.3	116	1	061001 mus musculu
16	1 NTC1_MOUSE	5.3	115	1	001705 mus musculu
17	1 NTC1_RAT	5.2	114.5	1	007008 rattus norv
18	1 NTC1_MOUSE	5.2	114	1	061554 mus musculu
19	1 LRP1_CHICK	5.1	112.5	1	098157 gallus gall
20	1 NTC1_HUMAN	5.1	112.5	1	P46531 homo sapien
21	1 LMG1_HUMAN	5.1	111.5	1	P11047 homo sapien
22	1 LMG1_HUMAN	5.1	111.5	1	P40798 drosophila
23	1 LRP1_HUMAN	5.0	110	1	007954 homo sapien
24	1 CRB_DROME	4.9	108	1	P10040 drosophila
25	1 G156_PAPPR	4.9	109	1	P13837 paramecium
26	1 FBNI_HUMAN	4.8	106	1	P33556 homo sapien
27	1 FBNI_HUMAN	4.8	105	1	P25304 rattus norv
28	1 FBNI_HUMAN	4.8	105	1	P98140 bos taurus
29	1 FBNI_MOUSE	4.8	105	1	061555 mus musculu
30	1 FBNI_HUMAN	4.8	105	1	P25591 homo sapien
31	1 LMG1_MOUSE	4.8	105	1	P02468 mus musculu
32	1 LMG1_MOUSE	4.7	104	1	P28799 homo sapien
33	1 GRN_HUMAN	4.7	103.5	1	001721 mus musculu
34	1 GRN_MOUSE	4.7	102.5	1	061982 mus musculu
35	1 YL_DROME	4.6	100.5	1	P98163 drosophila
36	1 LMG1_DROME	4.6	100	1	P15151 drosophila
37	1 GRN_MOUSE	4.5	99.5	1	P28797 caria porce
38	1 LRP2_HUMAN	4.5	98	1	P98164 homo sapien
39	1 LRP2_HUMAN	4.4	97	1	021313 caenorhabd1
40	1 LRP2_HUMAN	4.4	96.5	1	004833 caenorhabd1
41	1 LRP2_HUMAN	4.4	96	1	P14585 caenorhabd1
42	1 LRP2_HUMAN	4.4	95.5	1	061483 mus musculu
43	1 LRP2_HUMAN	4.4	95.5	1	P98155 homo sapien

RESULT	ID	Query Match Length	Score	DB	Description
1	1 NRTN_CHICK	25.9	568	1	013157 gallus gall
2	2 NRTN_MOUSE	24.9	544.5	2	008642 mus musculu
3	1 NRTN_HUMAN	24.7	540.5	1	000451 homo sapien
4	1 GDNF_CHICK	24.5	536.5	1	013156 gallus gall
5	1 GDNF_MOUSE	23.4	533	1	097785 mus musculu
6	1 GDNF_RAT	23.1	511	1	062997 rattus norv
7	1 GDNF_HUMAN	23.1	505.5	1	056159 homo sapien
8	1 NRTN_MOUSE	6.7	147	1	P07207 drosophila
9	1 NRTN_MOUSE	6.1	133.5	1	P19137 mus musculu
10	1 BARK_CHICK	5.7	124	1	003336 chironomus
11	1 FBNI_BOVIN	5.6	123.5	1	098133 bos taurus
12	1 FBNI_HUMAN	5.6	123.5	1	035555 homo sapien
13	1 NTC4_MOUSE	5.5	120	1	P31695 mus musculu
14	1 G168_PAPPR	5.4	117.5	1	P17053 paramecium
15	1 LMA5_MOUSE	5.3	116	1	061001 mus musculu
16	1 NTC1_MOUSE	5.3	115	1	001705 mus musculu
17	1 NTC1_RAT	5.2	114.5	1	007008 rattus norv
18	1 NTC1_MOUSE	5.2	114	1	061554 mus musculu
19	1 LRP1_CHICK	5.1	112.5	1	098157 gallus gall
20	1 NTC1_HUMAN	5.1	112.5	1	P46531 homo sapien
21	1 LMG1_HUMAN	5.1	111.5	1	P11047 homo sapien
22	1 LMG1_HUMAN	5.1	111.5	1	P40798 drosophila
23	1 LRP1_HUMAN	5.0	110	1	007954 homo sapien
24	1 CRB_DROME	4.9	108	1	P10040 drosophila
25	1 G156_PAPPR	4.9	109	1	P13837 paramecium
26	1 FBNI_HUMAN	4.8	106	1	P33556 homo sapien
27	1 FBNI_HUMAN	4.8	105	1	P25304 rattus norv
28	1 FBNI_HUMAN	4.8	105	1	P98140 bos taurus
29	1 FBNI_MOUSE	4.8	105	1	061555 mus musculu
30	1 FBNI_HUMAN	4.8	105	1	P25591 homo sapien
31	1 LMG1_MOUSE	4.8	105	1	P02468 mus musculu
32	1 LMG1_MOUSE	4.7	104	1	P28799 homo sapien
33	1 GRN_HUMAN	4.7	103.5	1	001721 mus musculu
34	1 GRN_MOUSE	4.7	102.5	1	061982 mus musculu
35	1 YL_DROME	4.6	100.5	1	P98163 drosophila
36	1 LMG1_DROME	4.6	100	1	P15151 drosophila
37	1 GRN_MOUSE	4.5	99.5	1	P28797 caria porce
38	1 LRP2_HUMAN	4.5	98	1	P98164 homo sapien
39	1 LRP2_HUMAN	4.4	97	1	021313 caenorhabd1
40	1 LRP2_HUMAN	4.4	96.5	1	004833 caenorhabd1
41	1 LRP2_HUMAN	4.4	96	1	P14585 caenorhabd1
42	1 LRP2_HUMAN	4.4	95.5	1	061483 mus musculu
43	1 LRP2_HUMAN	4.4	95.5	1	P98155 homo sapien

QY 182 YGACG-----GPHCRHNCRLRLTFEKAAPHAAGLLCPACANDRGERRNTIA 236
 DB 179 YISTCKEISATERRCHRRCKALROFEDVNPSEYTRILFCSC--KDOACAEPRROIV 236
 QY 237 PNCAL-PPVAPNCLERLRLCFSDPLCRSLVNDQTHCH-PMDLGTCAGAEQ-SRCIRATL 293
 DB 237 PCISYDKEKPNCLDLRNCRADHLCRLADHANCAQSPFSLTSCPDNTQACIGSYT 296
 QY 294 GLIGTAMTEPNVSNVTVALS--CTCRGSGNLQEECEMLGEPFHSNPLCTEAIKAKMF 351
 DB 297 GLIGFDMTNYVDASTTSLTSPSCSKSGNLECECFDNDFTENPCLRNALQAIFGNG 356
 QY 352 HSQLFSQDNPHPTFAVMAHONENPAV 377
 DB 357 TDVNLSPKNPSPPTIMLPYKESPAL 382
 RESULT 2
 NRTR_MOUSE STANDARD: PRT; 463 AA.
 008842;
 01-NOV-1997 (Rel. 35, Created)
 01-NOV-1997 (Rel. 35, Last sequence update)
 15-JUL-1999 (Rel. 38, Last annotation update)
 DE NEURTURIN RECEPTOR ALPHA PRECURSOR (NTRN-ALPHA) (NTRN-ALPHA) (TGF-
 DE BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 2) (GDNF RECEPTOR BETA)
 DE (GDNFR-BETA).
 GN GFRA2 OR GDNFRB OR TRNR2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97325791.
 RA BALOH R.H., TANSEY M.G., GOLDEN J.P., CREEDON D.J.,
 RA HECKEROTH R.O., KECK C.L., ZIMONJIC D.B., POPESCU N.C.,
 RA JOHNSON E.M. JR., MILBRANDT J.;
 RT "Trnr2, a novel receptor that mediates neurturin and GDNF signaling
 through Ret.";
 RL Neuron 18:793-802(1997).
 CC -1- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NTRN-INDUCED
 CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR. ALSO ABLE
 CC TO MEDIANE GDNF SIGNALING THROUGH THE RET TYROSINE KINASE
 CC RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
 CC SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS: A SHORT FORM IS PRODUCED BY ALTERNATIVE
 CC SPLICING.
 CC -1- TISSUE SPECIFICITY: NEURONS OF THE SUPERIOR CERVICAL AND DORSAL
 CC ROOT GANGLIA, AND ADULT BRAIN AND TESTIS. LOW LEVEL IN THE SPLEEN
 CC AND IN THE ADRENAL.
 CC -1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF002701; AAC53358.1; -
 CC DR MGD; MG1:1195462; GFRA2.
 CC KW Receptor; Glycoprotein; GPI-anchor; Membrane; Signal;
 CC Alternative splicing.
 CC FT SIGNAL 1 21
 CC FT CHAIN 22 443
 CC FT PROPEP 444 463
 CC FT CARBOHYD 52 52
 CC FT CARBOHYD 357 357
 CC FT CARBOHYD 413 413
 CC FT LIPID 443 443
 CC POTENTIAL.
 CC NEURTURIN RECEPTOR ALPHA.
 CC HYDROPHOBIC, REMOVED DURING MATURATION
 CC (POTENTIAL).
 CC POTENTIAL.
 CC POTENTIAL.
 CC GPI-ANCHOR (POTENTIAL).

FT VASPLIC 14 146 MISSING (IN SHORT FORM).
 SQ SEQUENCE 463 AA; 51598 MW; 0A2165C0 CR32;
 Query Match 24.9%; Score 544.5; DB 1; Length 463;
 Best Local Similarity 35.7%; Pred. No. 2,16-37;
 Matches 131; Conservative 48; Mismatches 141; Indels 47; Gaps 13;
 QY 44 CLQARKQADPTGSAAHNHDSCIS--SISTPLSEPSVPADCLAAQOLRNSLIGC 101
 DB 40 CVRAEILCAASNCSSRRYRLROCLAGDRNTMLANKE-----CQALEVLQESPLDQC 93
 QY 102 MCHRRKNVACLDIYTVHARBSLGNELDVSPEDYVTSKPMNLSKL----- 153
 DB 94 RCKRMKELOCLQIYNSIHGLIEGEFTYASPE-PYISR-----LSDIFRLASIFSG 147
 QY 153 ---NMLKPSDLCLKFAMLCTLNDKCDRLKAYGEAS-----GPHCRHNCRLRLTF 203
 DB 148 TGADPVYSAKSNHCLDAKACNLNDCKKLRSYSISICNREISPTERRNRRCKALRQF 207
 QY 204 FEKAEPHAAGLLCPACANDRGERRNTIAPNCL-PPVAPNCLERLRLCFSDPLCR 262
 DB 208 FDRVPSEYTYMLFCSC--QDOACAEPRROIVLSCSYDEKPKCLDLRSLCRTLHLCR 265
 QY 263 SRLVDFOTCHP--MDLIGTCAGOSCLRAYLLGIGAMPNPNVSNVTVALS--CTC 318
 DB 266 SRLADFPANCASTRITISCPADNYQACLGSIAMIGDMTPNTVDSNPIGIVVSPMCNC 325
 QY 319 RGSNGLQEECEMLGEPFHSNPLCTEAIKAKMFISQFSDMPH-PTFAVMAHONENPAV 377
 DB 326 RGSNMEBECEKFKDPTENDCLRNALQIA---FONGDVNNSPGRPIFSA---TOAPRV 378
 QY 378 RPOQWVP 384
 DB 379 EKTPSLP 385
 RESULT 3
 NRTR_HUMAN STANDARD: PRT; 464 AA.
 000451;
 01-NOV-1997 (Rel. 35, Created)
 01-NOV-1997 (Rel. 35, Last sequence update)
 15-JUL-1999 (Rel. 38, Last annotation update)
 DE NEURTURIN RECEPTOR ALPHA PRECURSOR (NTRN-ALPHA) (NTRN-ALPHA) (TGF-
 DE BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 2) (GDNF RECEPTOR BETA)
 DE (GDNFR-BETA).
 GN GFRA2 OR GDNFRB OR TRNR2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97325791.
 RA BALOH R.H., TANSEY M.G., GOLDEN J.P., CREEDON D.J.,
 RA HECKEROTH R.O., KECK C.L., ZIMONJIC D.B., POPESCU N.C.,
 RA JOHNSON E.M. JR., MILBRANDT J.;
 RT "Trnr2, a novel receptor that mediates neurturin and GDNF signaling
 through Ret.";
 RL Neuron 18:793-802(1997).
 CC -1- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NTRN-INDUCED
 CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR. ALSO ABLE
 CC TO MEDIANE GDNF SIGNALING THROUGH THE RET TYROSINE KINASE
 CC RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
 CC SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS: A SHORT FORM IS PRODUCED BY ALTERNATIVE
 CC SPLICING IN BOTH BRAIN AND PLACENTA.
 CC -1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.
 CC -----
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CC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-DORSAL ROOT GANGLION;
 RA WABE K.;
 CC Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED
 CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR (BY
 CC SIMILARITY).
 CC -1- SUBUNIT: 2 MOLECULES OF GDNF-ALPHA ARE THOUGHT TO FORM A COMPLEX
 CC WITH THE DISULFIDE-LINKED GDNF DIMER AND WITH 2 MOLECULES OF RET
 CC (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE GDNF FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AB000800; BAA19185.1;
 DR MGD; MGI:1100842; GPR1.
 KW Receptor; Glycoprotein; GPI-anchor; Membrane; Signal.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 430 GDNF RECEPTOR ALPHA.
 FT PROPEP 431 468 HYDROPHOBIC, REMOVED DURING MATURATION
 FT (POTENTIAL).
 FT DOMAIN 362 369 THR-RICH.
 FT CARBOHYD 59 59 POTENTIAL.
 FT CARBOHYD 347 347 POTENTIAL.
 FT CARBOHYD 406 406 POTENTIAL.
 FT LIPID 430 430 GPI-ANCHOR (POTENTIAL).
 SQ SEQUENCE 468 AA; 51782 MW; 6C64C182 CRC32;
 Query Match 23.4%; Score 513; DB 1; Length 468;
 Best Local Similarity 36.1%; Pred. No. 8e-35;
 Matches 130; Conservative 46; Mismatches 134; Indels 50; Gaps 13;
 QY 14 VMLLLPSPPLAAGDPLPTESRLMSCLARRCQADPTCSAAYHLDCTS---- 70
 DB 9 VLPDLILMSA--EYSGDRL-----DCVAKSDCLKEQSCSTYKTLRCCVAKKET 58
 QY 70 --SISTPLPSEPSVPADCLAAQOLNNSLIGCMCHRMKNQVACDIYVYHARSIG 127
 59 NFSLSGLEAND-----ECRSAMEALNKGSLYNCRCKRGMKKEKNCIRIYMSYQSLQ-G 112
 QY 128 NYELDVPYEDYVSKPWKANKLNLAKP-DSPL-----CLKFAMLCTLNDK 174
 DB 113 NDLEDEPYE-----EVSRLSDIFRAVPISDFEQVHISKGNCLDAAKANLDDT 166
 QY 175 CDRLKRYGEAC-----SGPHCORHYVCLROLLTFPEKAAEHAQGLLCPAPNDROGGER 230
 DB 167 CKYRSAYIIPCTTSMNENVCNKRKCKALROTFDKYPAHSGMLFCSC--RDVACTER 224
 QY 231 RRTIATNCALPP-VADNCLERLRCFSDPLCRSLVDFTQCHPMYD-IIGTCATEQ-SR 287
 DB 225 RROTIYVVCSEYERERENCLNLDSCIKYICSLADFTTNOQERSRVSNCLENYAD 284
 QY 288 CLRAYIGLITAMTPNPNVSNVYALSCRCRSGNLOECCEMLKEGFSHPCLTEIAIA 347
 DB 285 CLAYISGLITVMTPNYIDSSLSVAFWCCSSNGDLECLFLNFFKDNCTLAKNAIQ 344

RESULT 6
 GDNF-RAT
 ID GDNF-RAT STANDARD; PRT; 468 AA.
 AC 062957;
 DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE GDNF RECEPTOR ALPHA PRECURSOR (GDNF-RALPHA) (TGF-BETA RELATED
 GN NEUROTROPHIC FACTOR RECEPTOR 1) (RET LIGAND 1).
 GN GPR1 OR GDNFRA OR TRNR1 OR RETL1.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
 CC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-RETINA;
 RX MEDLINE; 96270513.
 RA JING S., WEN D., HU Y., HOLST P.L., LEO Y., FANG M., TAMIR R.,
 RA ANTONIO L., HU Z., COPPLES R., LOUIS J.-C., HU S., ALTHROCK B.W.,
 RA FOX G.M.;
 RT "GDNF-induced activation of the ret protein tyrosine kinase is
 RT mediated by GDNF-R-alpha, a novel receptor for GDNF."
 RL Cell 85:1113-1124(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MISTAR; TISSUE-KIDNEY;
 RX MEDLINE; 97322356.
 RA SANICOLA M., HESSON C.A., MORLEY D.S., CARMILO P., EHRENFELS C.,
 RA WATUS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
 RA PERINSKY R.B., CAPE R.L.;
 RT "Glial cell line-derived neurotrophic factor-dependent RET activation
 RT can be mediated by two different cell-surface accessory proteins."
 RL Proc. Natl. Acad. Sci. U.S.A. 94:6238-6243(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 96273032.
 RA TREANOR J.J.S., GOOGAN L., DE SAUVAGE F., STONE D.M., POULSEN K.T.,
 RA BECK C.D., GRAY C., ARMANINI M.P., POLLOCK R.A., HETTI F.,
 RA PHILLIPS H.S., GODDARD A., MOORE M.N., BUT-BELLO A., DAVIES A.M.,
 RA ASAI N., TAKAHASHI M., VANDLEN R., HENDERSON C.E., ROSENTHAL A.;
 RT "Characterization of a multicomponent receptor for GDNF."
 RL Nature 382:80-83(1996).
 CC -1- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED
 CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR.
 CC -1- SUBUNIT: 2 MOLECULES OF GDNF-ALPHA ARE THOUGHT TO FORM A COMPLEX
 CC WITH THE DISULFIDE-LINKED GDNF DIMER AND WITH 2 MOLECULES OF RET.
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER, BRAIN AND KIDNEY.
 CC -1- SIMILARITY: BELONGS TO THE GDNF FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; U59486; AAC52663.1;
 DR EMBL; U97142; AAC53300.1;
 KW Receptor; Glycoprotein; GPI-anchor; Membrane; Signal.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 430 GDNF RECEPTOR ALPHA.
 FT PROPEP 431 468 HYDROPHOBIC, REMOVED DURING MATURATION
 FT (POTENTIAL).
 FT DOMAIN 362 369 POLY-THR.
 FT CARBOHYD 59 59 POTENTIAL.
 FT CARBOHYD 347 347 POTENTIAL.
 FT CARBOHYD 406 406 POTENTIAL.
 FT LIPID 430 430 GPI-ANCHOR (POTENTIAL).
 SQ SEQUENCE 468 AA; 51649 MW; 6A7A2B2A CRC32;
 Query Match 23.3%; Score 511; DB 1; Length 468;
 Best Local Similarity 36.0%; Pred. No. 1.2e-34;
 Matches 130; Conservative 44; Mismatches 135; Indels 52; Gaps 13;
 QY 17 LMLLLPSPPLAAGDPLPTESRLMSCLARRCQADPTCSAAYHLDCTS---- 70

```

Db 6 LYFALPLDLMLSAEVSQDRL-----DCVKASDQCKECSCTKRTLRRCVAGKE 57
Oy 70 ---SISTPLPSEEPSPADCLPAQAOLRNSSLIGCKHRRKNQVACLDIYTVHARS 126
Db 58 TWFSLTSGLEAND-----ECRSAMEALKOKSLYNCRCKGKMKENKCLRIYWSMYOSLO 112
Oy 127 GNYELDVSPYEDVTYSKPKMKLSKLNMLKP-DSDL-----CLKFAMLCITLND 173
Db 112 GNDLLEDSPEYE-----PVNSRLSDIFRAVPISDVFOQVEHISKGNCLDAKACNLD 165
Oy 174 KCDRLRKAYGAGC-----SGPHQRHVCLROLITFEKKAEPHAGILLCPAPNDRCGE 229
Db 166 TCKKRSAYITPCTTSMSEVNCNRKCKHAKLROFFDKVPKHSYGMLCFCSC--RDICTE 223
Oy 230 RRRNTIAPNCALPP-VAPNCLRLCFSDPLCRSLVDVOTHCHPMD-ILGTCATEQ-S 286
Db 224 RRRQTIYVPCSYEERERNCGLSDSCRTNYICRSRLADFTTNCQPSRSYSNCLKENYA 283
Oy 287 RCLRAYLGLISTAMTPNPNVSNVTVALSCTCRSGSNLOECCMLEGFFSHNPLCTEIA 346
Db 284 DCLAYSGLIGTAVTWPNTIDSSLSVAPMCDSCNSGNDLECLFNLNFMDNCLKNAIQ 343
Oy 347 A 347
Db 344 A 344

```

RESULT 7

GNR_HUMAN STANDARD: PRT: 464 AA.

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AC P56159;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE GDNF RECEPTOR ALPHA PRECURSOR (GDNF-ALPHA) (IGF-BETA RELATED
  NEUROTROPHIC FACTOR RECEPTOR 1).
GN GFRAL OR GDNFRA OR TRNRI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
  Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SUBSTANTIA NIGRA;
RX JING S., WEN D., YU Y., HOLST P.L., LUD Y., FANG M., TAMIR R.,
  ANTONIO L., HU Z., CUPPLES R., LOUIS J.-C., HU S., ALTRICK B.W.,
  FOX G.M.;
  "GDNF-induced activation of the ret protein tyrosine kinase is
  mediated by GDNF-alpha, a novel receptor for GDNF.";
  Cell 85:113-1124(1996).
CC -1- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED
  AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR (BY
  SIMILARITY).
CC -1- SUBUNIT: 2 MOLECULES OF GDNF-ALPHA ARE THOUGHT TO FORM A COMPLEX
  WITH THE DISULFIDE-LINKED GDNF DIMER AND 2 MOLECULES OF RET (BY
  SIMILARITY).
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
  SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE GDNF FAMILY.
CC -1- SIMILARITY: BELONGS TO THE GDNF FAMILY.
DR MIM: 601496;
KW Receptor; Glycoprotein; GPI-anchor; Membrane; Signal.
FT SIGNAL 25 428
FT CHAIN 1 24
FT PROPEP 429 464
FT 361 368
FT CARBOHYD 39 39
FT CARBOHYD 346 346
FT CARBOHYD 405 405
FT LIPID 428 428
SO SEQUENCE 464 AA; 51291 MW; 2C8C574 CRC32;

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Query Match 23.1%; Score 505.5; DB 1; Length 464;
 Best Local Similarity 36.3%; Pred. No. 3.3e-34;
 Matches 131; Conservative 45; Mismatches 132; Indels 53; Gaps 14;

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Oy 17 LILLIPSPPLPAA---GDPLPTESRIMNSCLQARRCQADPTCSAYNHIDSCTS--- 70
Db 6 LYFALPLDLMLSAEVSQDRL-----DCVKASDQCKECSCTKRTLRRCVAGKE 57
Oy 70 ---SISTPLPSEEPSPADCLPAQAOLRNSSLIGCKHRRKNQVACLDIYTVHARS 126
Db 58 TWFSLTSGLEAND-----ECRSAMEALKOKSLYNCRCKGKMKENKCLRIYWSMYOSLO 112
Oy 127 GNYELDVSPYEDVTYSKPKMKLSKLNMLKP-DSDL-----CLKFAMLCITLND 173
Db 112 GNDLLEDSPEYE-----PVNSRLSDIFRAVPISDVFOQVEHISKGNCLDAKACNLD 165
Oy 174 KCDRLRKAYGAGC-----SGPHQRHVCLROLITFEKKAEPHAGILLCPAPNDRCGE 229
Db 166 TCKKRSAYITPCTTSMSEVNCNRKCKHAKLROFFDKVPKHSYGMLCFCSC--RDICTE 223
Oy 230 RRRNTIAPNCALPP-VAPNCLRLCFSDPLCRSLVDVOTHCHPMD-ILGTCATEQ-S 286
Db 224 RRRQTIYVPCSYEERERNCGLSDSCRTNYICRSRLADFTTNCQPSRSYSNCLKENYA 283
Oy 287 RCLRAYLGLISTAMTPNPNVSNVTVALSCTCRSGSNLOECCMLEGFFSHNPLCTEIA 346
Db 283 DCLAYSGLIGTAVTWPNTIDSSLSVAPMCDSCNSGNDLECLFNLNFMDNCLKNAIQ 342
Oy 347 A 347
Db 343 A 343

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RESULT 8

NOTC_DROME STANDARD: PRT: 2703 AA.

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AC P07207; P04154;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE "Nucleotide sequence from the neurogenic locus notch implies a gene
  product that shares homology with proteins containing EGF-like
  repeats.";
  Cell 43:567-581(1985).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-OREGON-R;
RX MEDLINE: 87064624.
RA KIDD S., KELLEY M.R., YOUNG M.W.;
  "Sequence of the notch locus of Drosophila melanogaster: relationship
  of the encoded protein to mammalian clotting and growth factors.";
  Mol. Cell. Biol. 6:3094-3108(1986).
RN [3]
RP SEQUENCE OF 2505-2611 FROM N.A.
RX MEDLINE: 85099329.
RA WHARTON K.A., YEDOVONICK B., FINNERTY V.G., ARTAVANIS-TSAKONAS S.;
  "opa: a novel family of transcribed repeats shared by the Notch locus
  and other developmentally regulated loci in D. melanogaster.";
  Cell 40:55-62(1985).
RN [4]
RP SEQUENCE OF 1-8 FROM N.A.
RX MEDLINE: 87257846.

```


R:Kidd, S.; Kelley, M.R.; Young, M.N.
 Mol. Cell. Biol. 6, 3094-3108, 1986
 A:Reference number: A24420; MUID:87064624
 A:Accession: A24420
 A:Molecule type: DNA
 A:Residues: 1-2703 <KID>
 A:Cross-references: GB:R03508; NID:q157991; PIRN:AAA28725.1; PID:q157993
 R:Marion, K.A.; Johansen, K.M.; Xu, T.; Artaanis-Tsakonas, S.
 Cell 43, 567-581, 1985
 A:Reference number: A24768; MUID:86079539
 A:Accession: A24768
 A:Molecule type: mRNA
 A:Residues: 1-48; '1', 50-118; 'R', 120-230; 'T', 232-256; 'N', 258-266; 'A', 268-872; 'R', 874-958;
 R:Note: the authors translated the codon ATC for residue 49 as Thr, ATT for residue 2044
 R:Note: D.
 Nucleic Acids Res. 17, 6463-6471, 1989
 A:Title: Hypervariability of simple sequences as a general source for polymorphic DNA ma
 A:Reference number: S09358; MUID:89385974
 A:Accession: S09358
 A:Molecule type: DNA
 A:Residues: 2505-2551; 'QQQ', 2552-2576; 'E', 2578-2604 <TAU>
 R:Marion, K.A.; Yedvobnick, B.; Finnerty, V.G.; Artaanis-Tsakonas, S.
 Cell 40, 55-62, 1985
 A:Title: opa: a novel family of transcribed repeats shared by the Notch locus and other
 A:Reference number: A05267; MUID:85093329
 A:Accession: A05267
 A:Molecule type: DNA
 A:Residues: 2504-2576; 'E', 2578-2611 <WHA2>
 C:Genetics:
 A:Gene: notch; opa
 A:Cross-references: FlyBase:FBgn0004647
 A:Map position: 8.96-9.36
 A:Insertion: 53/3; 84/3; 171/3; 240/3; 283/3; 233/3; 2436/3; 2588/3
 C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
 C:Keywords: differentiation; tandem repeat; transmembrane protein
 F:27-43/Domain: transmembrane #status predicted <TM1>
 F:297-328/Domain: EGF homology <EGF1>
 F:530-561/Domain: EGF homology <EGF1>
 F:568-599/Domain: EGF homology <EGF>
 F:988-1018/Domain: EGF homology <EGF2>
 F:1064-1095/Domain: EGF homology <EGF3>
 F:1187-1218/Domain: EGF homology <EGF3>
 F:1746-1762/Domain: transmembrane #status predicted <TM2>
 F:1950-1982/Domain: ankyrin repeat homology <AN1>
 F:1983-2015/Domain: ankyrin repeat homology <AN2>
 F:1988-2004/Domain: transmembrane #status predicted <TM3>
 F:2012-2049/Domain: ankyrin repeat homology <AN3>
 F:2050-2082/Domain: ankyrin repeat homology <AN4>
 F:2083-2115/Domain: ankyrin repeat homology <AN5>
 F:238-2568/Region: glutamine-rich
 F:2538-2568/Domain: neurogenic repetitive element #status predicted <OPA>
 Query Match 7.3%; Score 147.5; DB 1; Length 2703;
 Best Local Similarity 20.9%; Pred. No. 0.001;
 Matches 82; Conservative 37; Mismatches 120; Indels 153; Gaps 22;
 QY 41 MNSCLARRKQADPTCSAYHLDCTSSISTPL-----PSEPSVPADCTEAAQ 92
 DB 985 INECIS--QPCNGATCS--QVNSYCT-----CPIGFSGINQTNDEDTSSCLNGGSC 1037
 QY 93 L-----NNSLIGCMCR----- 106
 DB 1038 IINGINGNCISLAGYSGANCOYKLNKCDNPNCLNGATCHEONNEYTCHEPSGFTGKQCE 1097
 QY 106 -----RAKNQVAC-LDYVTWTHARASLSDSLC-----L 132
 DB 1098 YDWMGQSPCENGATCSQKHKHPSCKSGSGWT-----GTLCDVYTISCDADADRGL 1149
 QY 133 KRAMLCTLNKCDRLKAYGEA-----CS-----GPHCORRV-----CLRLQLTF 172
 DB 1150 SLROLCLN-NGTC-----KDYGNHVCYCSGSGYAGSYCQKREIDSCQSPQONGSTCHDLIGA 1204

QY 173 FEKRAEPHAG-----LLPCCAPN--DRG--CGERRRNTIAPNCALPVAPNCL-ELRR- 223
 DB 1205 YEQQCGHGFQNGCNELNIDDCAPNPQNGNGTCHDRMNF---SCSPPTMTGICINKD 1261
 QY 223 -----LCFSDPLCRSLVDVQTHCHPMDLTGTCATGQSRCLRAYLGLTAMTPNEVSNV 277
 DB 1262 DCRPGACHNNGSCIDRVGGEFCVCPGFVGARCEGIDNCLNPNCSNAGTLDCVQLVNNY 1321
 QY 278 NTSVALSCTRGSGNQECCMLEGFEFSHNP 309
 DB 1322 H-----CNCR-PGHMGRHCHKVDPCASPC 1346
 RESULT 3
 A47221
 fibrillin 1 precursor - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 02-Jun-1995 #sequence_revision 25-Apr-1997 #text_change 13-Aug-1999
 C:Accession: A47221; I54355; S17064; I59574; S17062; S6211; A34198
 R:Corson, G.M.; Chabberg, S.C.; Dietz, H.C.; Charbonneau, N.L.; Sakai, L.Y.
 Genomics 17, 476-484, 1993
 A:Title: Fibrillin binds calcium and is coded by cDNAs that reveal a multidomain stru
 A:Reference number: A47221; MUID:94010947
 A:Accession: A47221
 A:Molecule type: mRNA
 A:Residues: 1-337; 'T', 339-1029 <COR>
 A:Cross-references: GB:X63556
 R:Perletti, L.V.; D'Alessio, M.; Ramirez, F.; Lynch, J.; Sykes, B.; Pangillan, T.; Bo
 Hum. Mol. Genet. 2, 961-968, 1993
 A:Title: Genomic organization of the sequence coding for fibrillin, the defective gen
 A:Reference number: I54355; MUID:93372860
 A:Accession: I54355
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 132-3002 <PER>
 A:Cross-references: GB:LI3923; NID:9306745; PID:9306746
 R:Malet, C.L.; Corson, G.M.; Maddox, B.K.; Glanville, R.W.; Sakai, L.Y.
 Nature 352, 334-337, 1991
 A:Title: Partial sequence of a candidate gene for the Marfan syndrome.
 A:Reference number: S17064; MUID:91304568
 A:Accession: S17064
 A:Molecule type: mRNA
 A:Residues: 1030-3002 <MAS>
 A:Cross-references: EMBL:X63556
 R:Dietz, H.C.; Valle, D.; Francomano, C.A.; Kendzior, R.J.
 Science 259, 680-683, 1993
 A:Title: The skipping of constitutive exons in vivo induced by nonsense mutations.
 A:Reference number: I59574; MUID:93157831
 A:Accession: I59574
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 2217-2288; 'T', 2290-2325 <RES>
 A:Cross-references: GB:S54426; NID:9264860; PID:9264861
 R:Lee, B.; Godfrey, M.; Vitale, E.; Hori, H.; Mattei, M.G.; Sarfarazi, M.; Tsipouras,
 Nature 352, 330-334, 1991
 A:Title: Linkage of Marfan syndrome and a phenotypically related disorder to two diff
 A:Reference number: S17062; MUID:91304567
 A:Accession: S17062
 A:Molecule type: mRNA
 A:Residues: 'VAVTVFIFLSYKML', 944-1444 <LEE1>
 A:Cross-references: EMBL:X62008
 A:Accession: S62111
 A:Molecule type: Protein
 A:Residues: 1166-1176; 'X', 1178-1180; 'D', 1182-1185 <LEE2>
 R:Maddox, B.K.; Sakai, L.Y.; Keene, D.R.; Glanville, R.W.
 J. Biol. Chem. 264, 21381-21385, 1989
 A:Title: Connective tissue microfibrils. Isolation and characterization of three larg
 A:Reference number: A34198; MUID:90078246
 A:Accession: A34198
 A:Molecule type: Protein
 A:Residues: 585-575; 1890-1892; 'T', 1894-1900 <MAD>
 C:Comment: Fibrillin is a major component of elastin-associated microfibrils.
 C:Genetics:

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 13, 1999, 02:45:08 ; Search time 20.22 Seconds

(without alignments)
530.797 Million cell updates/sec

Title: US-09-272-835-17

Perfect score: 2022

Sequence: 1 MVRNLRNPRLPPVLMILL.....PMVPSLSECTPLILLISLW 369

Scoring table: BLOSUM62

Searched: 80000 seqs, 29085965 residues

Database: SWISSPROT_38:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	538.5	26.6	465	1	NTRR_CHICK
2	513	25.4	463	1	NTRR_MOUSE
3	509	25.2	464	1	NTRR_HUMAN
4	503	24.9	469	1	GDNR_CHICK
5	485.5	24.0	468	1	GDNR_MOUSE
6	483.5	23.9	468	1	GDNR_MOUSE
7	475	23.5	466	1	GDNR_RAT
8	475	23.5	466	1	GDNR_RAT
9	147.5	7.3	2703	1	NOTC_HUMAN
10	126	6.2	2871	1	NOTC_DROME
11	124	6.2	2871	1	FBN1_BOVIN
12	124	6.1	2704	1	FBN1_HUMAN
13	123	6.1	3084	1	G168_PARP
14	122.5	6.1	1964	1	LMG1_MOUSE
15	121	6.0	2444	1	NTC4_MOUSE
16	117.5	5.8	2715	1	NTC1_HUMAN
17	117	5.8	384	1	G156_PARP
18	114.5	5.7	2139	1	GAS1_MOUSE
19	114.5	5.7	2531	1	CRB_DROME
20	112.5	5.6	1959	1	NTC1_MOUSE
21	111.5	5.5	2911	1	AGRI_RAT
22	110.5	5.5	593	1	FBN2_HUMAN
23	110.5	5.5	3635	1	GRN_HUMAN
24	110	5.4	2907	1	LMAS_MOUSE
25	110	5.4	1609	1	FBN2_MOUSE
26	107.5	5.4	2871	1	LMG1_HUMAN
27	107.5	5.3	1639	1	FBN1_MOUSE
28	107.5	5.3	2437	1	LMG1_DROME
29	107	5.3	2318	1	NOTC_BRAR
30	106.5	5.3	1700	1	NTC3_MOUSE
31	106.5	5.3	566	1	Y1_DROME
32	106.5	5.3	601	1	BAR3_CHITE
33	106.5	5.3	683	1	FBLB_HUMAN
34	106.5	5.3	703	1	FBLB_HUMAN
35	106	5.2	4660	1	FBLD_HUMAN
36	106	5.2	2531	1	LRP2_RAT
37	105.5	5.2	345	1	NTC1_RAT
38	105.5	5.2	1767	1	CAS1_HUMAN
39	105.5	5.2	1607	1	LMG1_MOUSE
40	105.5	5.2	4544	1	LMG1_MOUSE
41	104.5	5.2	593	1	LRP1_HUMAN
42	103	5.1	4543	1	FA12_BOVIN
43	102.5	5.1	3672	1	LRP1_CHICK
					LMG2_CABEL

ALIGNMENTS

44	102.5	5.1	4655	1	LRP2_HUMAN	P98164	homo sapien
45	102	5.0	591	1	GRN_CAVPO	P28797	cavia porce

ALIGNMENTS

RESULT	1																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					</
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157 -----GPHCHVCLRLTFFEKAAEPHAGGLICPCAPNDROGGERRTIAPNCAL- 211
 DB 185 KEISHTHCSSRRKCHKAIRPFDDNPVSEYTRLLFCSC--KDAQCAEPRRQTIYPCFSYE 242
 QY 211 PPVAPNCLIELRLCFSDPCLSRVLDPFOTCH-PMDILGTCATEQ-SRCLRAYLGLIGTA 268
 DB 243 DKRPNCIDLRNVCADHLCRSRLADFHANQASFOQLSCPGNYOACLSYGLIGFD 302
 QY 269 MTPNPVSVNTSVALS--CTCRGSGNLQEECEMTEGGFSSNHPCLTEAIANRPHSOLFS 326
 DB 303 MTPNPVASTSTITISPCWCKSGGNEECCKELRDTFENPCLRNIAIOAFNGDYNLS 362
 QY 327 QDWHPTEFAVAHONENPAV 346
 DB 363 PKNPSPTMLPKYKESPAL 382
 RESULT 2
 NRTN_MOUSE STANDARD: PRT: 463 AA.
 008842:
 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE NEURTURIN RECEPTOR ALPHA PRECURSOR (NTRN-ALPHA) (NTRN-ALPHA) (TGF-
 DE BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 2) (GDNF RECEPTOR BETA)
 DE (GDNF-BETA)
 GN GFRA2 OR GDNFRB OR TRNR2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX BALOH R.H., TANSEY M.G., GOLDEN J.P., CREEDON D.J.,
 RA HEUCKEROFF R.O., KECK C.L., ZIMONJIC D.B., POPESCU N.C.,
 RA JOHNSON E.M. JR., MILBRANDT J.;
 RT "Trnr2, a novel receptor that mediates neurturin and GDNF signaling
 RT through Ret.";
 RL Neuron 18:793-802(1997).
 CC -1- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NRTN-INDUCED
 CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR. ALSO ABLE
 CC TO MEDIANE GDNF SIGNALING THROUGH THE RET TYROSINE KINASE
 CC RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
 CC SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS: A SHORT FORM IS PRODUCED BY ALTERNATIVE
 CC SPLICING.
 CC -1- TISSUE SPECIFICITY: NEURONS OF THE SUPERIOR CERVICAL AND DORSAL
 CC ROOT GANGLIA, AND ADULT BRAIN AND TESTIS. LOW LEVEL IN THE SPLEEN
 CC AND IN THE ADRENAL.
 CC -1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL, AF002701; AAC53548.1;
 DR MGD; MGI:1195462; GFRA2.
 KW Receptor; Glycoprotein; GPI-anchor; Membrane; Signal;
 KM Alternative splicing.
 FT SIGNAL 1 21
 FT CHAIN 22 443
 FT PROPEP 444 463
 FT CARBOHYD 52 52
 FT CARBOHYD 357 357
 FT CARBOHYD 413 413
 FT LIPID 443 443
 FT GPI-ANCHOR (POTENTIAL).
 FT POTENTIAL.
 FT REMOVED DURING MATURATION
 FT POTENTIAL.
 FT POTENTIAL.
 FT POTENTIAL.
 FT GPI-ANCHOR (POTENTIAL).

FT VARSPLIC 14 146 MISSING (IN SHORT FORM).
 SQ SEQUENCE 463 AA; 51598 MW; 0A2165C0 CRC32;
 Query Match 25.4%; Score 513; DB 1; Length 463;
 Best Local Similarity 33.8%; Pred. No. 2,6e-35;
 Matches 122; Conservative 42; Mismatches 131; Indels 66; Gaps 11;
 QY 44 CLOARRKQADPTCSAAYHLDSCST--SISTLPSESPVADPCLEAQQLNSSLIGC 101
 DB 40 CVANELCALESNCSSRYRLRCLAGRNMTLANKE-----CQALEVLDSPPLYDC 93
 QY 102 MCHRRKNOVACDITWYHAR----- 125
 DB 94 RCRGRKKELQCIQIYWSHILGTEGEFEYAEPEPYTSRLSDIFRLASIFSGADPV 153
 QY 125 -SLDSCLKFAMLCTLNKCDRLKAYGEACS-----GPHCHVCLRLTFFEKAAE 178
 DB 154 VSAKSNHCLDPAACNLNCKRLRSSYISICNREISPTERCNRRCHRALRQFFRVPS 213
 QY 179 PHAAGLLCPCAPNDROGGERRTIAPNCAL-PPVAPNCLIELRLCFSDPCLSRSLYDP 237
 DB 214 EYTYRLFCSC--QDACAEPRRQTIYPCSCSYDEKPKCLDLSCRTDHLCRSLADP 271
 QY 238 QTRCHP--MDILGTCATEQSRCLRAYLGLIGTAMPEFVSNTSVALS--CTCRGSGNL 293
 DB 272 HANCRASYRTITSCPADNTQACIGSYAGMIGDMFNEDNSPTGIVSPKCRSGSN 331
 QY 294 QEECEMTEGGFSSNHPCLTEAIANRPHSOLFSQDMPH-PTAVAHONENPAVRPOPVY 352
 DB 332 EEECEMTEGGFSSNHPCLTEAIANRPHSOLFSQDMPH-PTAVAHONENPAVRPOPVY 384
 QY 353 P 353
 DB 385 P 385
 RESULT 3
 NRTN_HUMAN STANDARD: PRT: 464 AA.
 ID NRTN_HUMAN 000451:
 AC 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE NEURTURIN RECEPTOR ALPHA PRECURSOR (NTRN-ALPHA) (NTRN-ALPHA) (TGF-
 DE BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 2) (GDNF RECEPTOR BETA)
 DE (GDNF-BETA)
 GN GFRA2 OR GDNFRB OR TRNR2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX BALOH R.H., TANSEY M.G., GOLDEN J.P., CREEDON D.J.,
 RA HEUCKEROFF R.O., KECK C.L., ZIMONJIC D.B., POPESCU N.C.,
 RA JOHNSON E.M. JR., MILBRANDT J.;
 RT "Trnr2, a novel receptor that mediates neurturin and GDNF signaling
 RT through Ret.";
 RL Neuron 18:793-802(1997).
 CC -1- FUNCTION: RECEPTOR FOR NEURTURIN. MEDIATES THE NRTN-INDUCED
 CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR. ALSO ABLE
 CC TO MEDIANE GDNF SIGNALING THROUGH THE RET TYROSINE KINASE
 CC RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
 CC SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS: A SHORT FORM IS PRODUCED BY ALTERNATIVE
 CC SPLICING IN BOTH BRAIN AND PLACENTA.
 CC -1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AF002700; AAC52036.1; -
 DR MIM: 601956; -
 KW Receptor; Glycoprotein; GPI-anchor; Membrane; Signal;
 KW Alternative splicing.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 444 NEUTRIN RECEPTOR ALPHA.
 FT PROPEP 445 464 HYDROPHOBIC, REMOVED DURING MATURATION
 FT CARBOHYD 52 52 (POTENTIAL).
 FT CARBOHYD 357 357 (POTENTIAL).
 FT CARBOHYD 413 413 POTENTIAL.
 FT LIPID 444 444 GPI-ANCHOR (POTENTIAL).
 FT VARPPLIC 14 14 MISSING (IN SHORT FORM).
 FT SEQUENCE 464 AA; 51558 MW; 3C74BBB CRC32;
 Query Match 25.2%; Score 509; DB 1; Length 464;
 Best Local Similarity 34.4%; Pred. No. 5.5e-35;
 Matches 111; Conservative 41; Mismatches 113; Indels 58; Gaps 8;
 Oy 44 CLOARRCOADPTCSAAYHHLDSCTS--SISTPLSEEPSPADCLEAQAOLNSSLIGC 101
 Db 40 CVRAMELCAESCSRYTLRCLAGRDNTLANKE-----COALEVLOESPLYDC 93
 Oy 102 MCHRRKNVACLDITYVYHRA----- 125
 Db 94 RCKRKKKELOCIQIYWSIHLGTEGEFEYEAAPYVTSRLSDIFRLASIFSGTADPY 153
 Oy 125 -SLDSDLCKFPMMLCTLNKCDRLKRAYGEAC-----GPHCRHVCLOLTFEKKAE 178
 Db 154 VSASKNHCLDAKACALNCKKRLSSYSICNREISPERCKRRCKHAKLRFEPDVS 213
 Oy 179 PHAGILLPCAPANDRGCGERRRTIAPNCAL-PPVAPNCLRLRCLFSPDLGRSLYDF 237
 Db 214 EYTYMMLFSC--QOACERRROTILPSCSYEDKPKNCLDGVCRDHLCRSLADP 271
 Oy 238 OTHCHP--MDIGTCATEGSCRLRAYLIGTAMPNPNVNTVALS--CTCRSGNL 293
 Db 292 HANCRASYOTVTSADPNQACISYAGMIGFDMPTNYDSSPTGLVSPMCSGSGNM 331
 Oy 294 OECECMLEGFESHNPCLTEPAIA 316
 Db 332 EECERFLDFTEPNCLRNAIOA 354
 RESULT 4
 GDNF_CHICK STANDARD: PRT; 469 AA.
 ID GDNF_CHICK
 AC 013156;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF-BETA RELATED
 DE NEUROTROPIC FACTOR RECEPTOR 1).
 DE GFRAL OR GDNFRA.
 OS Gallus gallus (Chicken).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
 OS Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN.
 RC MEDLINE; 97336104.
 RA BUY-BELLO A., ADU J., PINON L.G.P., HORTON A., THOMPSON J.,
 RA ROSENTHAL A., CHINCHETRU M., BUCHANAN V.L., DAVIES A.M.;
 RA "Neuritin responsiveness requires a GPI-linked receptor and the Ret
 RA receptor tyrosine kinase".
 RA Nature 387:721-724(1997).
 CC -1- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED

CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR (BY
 CC SIMILARITY).
 CC -1- SUBUNIT: 2 MOLECULES OF GDNFR-ALPHA ARE THOUGHT TO FORM A COMPLEX
 CC WITH THE DISULFIDE-LINKED GDNF DIMER AND WITH 2 MOLECULES OF RET
 CC (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE GDNFR FAMILY.
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 CC -----
 DR EMBL: U90541; AAB61570.1; -
 DR Receptor; Glycoprotein; GPI-anchor; Membrane; Signal.
 KW Receptor; Glycoprotein; GPI-anchor; Membrane; Signal.
 FT SIGNAL 1 27 POTENTIAL.
 FT CHAIN 28 430 GDNF RECEPTOR ALPHA.
 FT PROPEP 431 469 HYDROPHOBIC, REMOVED DURING MATURATION
 FT DOMAIN 361 368 POLY-THR.
 FT CARBOHYD 62 62 POTENTIAL.
 FT CARBOHYD 163 163 POTENTIAL.
 FT CARBOHYD 346 346 POTENTIAL.
 FT CARBOHYD 405 405 POTENTIAL.
 FT LIPID 430 430 GPI-ANCHOR (POTENTIAL).
 FT SEQUENCE 469 AA; 52043 MW; C8D241C9 CRC32;
 Query Match 24.9%; Score 503; DB 1; Length 469;
 Best Local Similarity 35.3%; Pred. No. 1.7e-34;
 Matches 123; Conservative 42; Mismatches 127; Indels 56; Gaps 11;
 Oy 16 MLLLLPSPPLIAG-DPLPESRLMSCLDARRKCOADPTCSAAYHHLDSCTS----- 70
 Db 5 LLYLALPLADVLLSAEVSGLPGDRL--DCVAKASDCKLEKSCSTKYTLRLQCVAGKESN 62
 Oy 70 -SISTPLSEEPSPADCLEAQAOLNSSLIGCMHRRKNVACLDITYVYHRA----- 124
 Db 63 FSRATGLEKD-----ECKSAMKALKOSLYNCRKRGKKEKNCILRYWSYOSLGND 117
 Oy 124 -----RSLSDL-----CLFAMLCITLDCDRLKRAYGEAC 155
 Db 118 LLEDSPYEPVNSRLSDIFRLAIVSEVPLVSGNCCDLAARACNLNDCKFRSAIYTPC 177
 Oy 156 -----SGPHCRVHCLRLQTLTFEKAEPHAGLLICPCAPNDRGCGERRRTIAPNCALP 211
 Db 178 TSTSTNEICNKKRCKALRLEFDKVPKHSYGMFLCSC--RDVACTERRROTIVVCSYE 235
 Oy 212 P-VAPNCLRLRCLSDPLCRSLYDPOTHCPMD-IIGTCATED-SICLAYLGLITA 268
 Db 236 DREKNCNLDSCKKNTICSLRLDFTNCPESRVSLSCKEYACCLLAYSGLIGTV 295
 Oy 269 MTPNFVSNVNTVALSCTCRSGNLQEECEMLEGFFSHNPCLTEPAIA 316
 Db 296 MTPNIDSSLSVAPMWCDSNGNDIDECRFLNFPODNTLKNALIOA 343
 RESULT 5
 GDNF_MOUSE STANDARD: PRT; 468 AA.
 ID GDNF_MOUSE
 AC P97785;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF-BETA RELATED
 DE NEUROTROPIC FACTOR RECEPTOR 1).
 DE GFRAL OR GDNFRA OR TRNRL.
 OS Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1] SEQUENCE FROM N.A.
 RP TISSUE-DORSAL ROOT GANGLION;
 RC WATABE K.;
 RA Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 RL -1- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED
 CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR (BY
 CC SIMILARITY).
 CC -1- SUBUNIT: 2 MOLECULES OF GDNF-ALPHA ARE THOUGHT TO FORM A COMPLEX
 CC WITH THE DISULFIDE-LINKED GDNF DIMER AND WITH 2 MOLECULES OF RET
 CC (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
 CC SIMILARITY). BELONGS TO THE GDNF FAMILY.
 CC -1- SIMILARITY: BELONGS TO THE GDNF FAMILY.
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 CC
 DR EMBL: AB000800; BAF19185.1; -
 DR MGD: MGI:1100842; GFRAL.
 KW Receptor; Glycoprotein; GPI-anchor; Membrane; signal.
 FT SIGNAL 1 24
 FT CHAIN 25 430 GDNF RECEPTOR ALPHA.
 FT PROPEP 431 468 HYDROPHOBIC, REMOVED DURING MATURATION
 FT (POTENTIAL).
 FT DOMAIN 362 369 THR-RICH.
 FT CARBOHYD 359 359 POTENTIAL.
 FT CARBOHYD 347 347 POTENTIAL.
 FT CARBOHYD 406 406 POTENTIAL.
 FT LIPID 430 430 GPI-ANCHOR (POTENTIAL).
 SO SEQUENCE 468 AA; 51782 MW; 6C64C182 CRC32;

Query Match 24.0%; Score 485.5; DB 1; Length 468;
 Best Local Similarity 34.3%; Pred. No. 4.8e-33;
 Matches 121; Conservative 42; Mismatches 123; Indels 67; Gaps 11;

14 VMLLLPSPPLAAGDPLPESRLMNSCLARRKCAQDPGSAAYHHLDSCS---70
 9 VLPLDLMLNSA-EVSGGRL-----DCVRAADQCLKEGSCSKYRLRQCVAGKET 58
 70 -SISPLPEEPSPADCLAAQOLRNSLLICMCHRRKNVACLDIYTH-----122
 59 NPLTSLGLEAKD-----ECNSAEALAKOKSLYNCRCRGRKKRKNCLRTIYWSYQSLQGN 113
 122 -----PARSLDSDL-----CLKFAMLCTLNDKDLRKA 150
 114 DLLEDSPEYEVNRLSDIFRAVPIFISDYQOVVHISKGNKNCDAARACHLDQCKRYRRA 173
 151 YGSAAC-----SGPRQAHVCLROLTLTFEFAAEPAHAGLLCPAPDRGCGERRNTIAP 206
 174 YTPCTTSNSNEVCNRRKCKHKLROFFDKYPAKHSYGMFCSC--RDVACTERRQITIP 231
 207 NCALPP-VAPNCLERLRICEPDLGRSLVDYDPTCHPMQ-ILGTATATQ-SRCLRAYTG 263
 232 VCSYERERENCLNTDSCATNTICRSRLADFTNCPQPSRSVSNCLKENTYADCLLAYSG 291
 264 LIGTATPNTFVSNVNTVALSCTCRGSGNLQEECEMLLEFFSNPCLTAIAA 316
 292 LIGTATPNTFVSNVNTVALSCTCRGSGNLQEECEMLLEFFSNPCLTAIAA 344

RESULT 6
 GDNF_RAT
 ID GDNF_RAT STANDARD; PRT; 468 AA.
 AC 062397;
 DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE GDNF RECEPTOR ALPHA PRECURSOR (GDNF-ALPHA) (TGF-BETA RELATED
 DE NEUROTROPHIC FACTOR RECEPTOR 1) (RET LIGAND 1).
 GN GFRAL OR GDNFRA OR TNRI OR RETL.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
 CC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1] SEQUENCE FROM N.A.
 RP TISSUE-RETINA.
 RC MEDLINE: 96270513.
 RA JING S., WEN D., YU Y., HOLST P.L., LUO Y., FANG M., TAMIR R.,
 RA ANTONIO L., HU Z., CUPPLES R., LOUIS J.-C., HU S., ALTHROCK B.W.,
 RA FOX G.M.;
 RT "GDNF-induced activation of the ret protein tyrosine kinase is
 RT mediated by GDNF-alpha, a novel receptor for GDNF."
 RL Cell 85:1113-1124(1996).
 RN [2] SEQUENCE FROM N.A.
 RP STRAIN-MISTAR; TISSUE-KIDNEY;
 RC MEDLINE: 97323356.
 RA SANTOCLA M., HESSION C.A., WORLEY D.S., CARNILLO P., EHRENFELS C.,
 RA WALDS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
 RA PEPINSKY R.B., CATE R.L.;
 RT "Glial cell line-derived neurotrophic factor-dependent RET activation
 RT can be mediated by two different cell-surface accessory proteins."
 RL Proc. Natl. Acad. Sci. U.S.A. 94:6238-6243(1997).
 RN [3] SEQUENCE FROM N.A.
 RP MEDLINE: 96273032.
 RA TREANOR J.J.S., GOOGMAN L., DE SAUVAGE F., STONE D.M., POULSEN K.T.,
 RA BECK C.D., GRAY C., ARMANINI M.P., POLLOCK R.A., HEFT F.,
 RA PHILLIPS H.S., GODDARD A., MOORE M.W., BOUT-BELLO A., DAVIES A.M.,
 RA ASAI N., TAKAHASHI M., VANDLEN R., HENDERSON C.E., ROSENTHAL A.;
 RT "Characterization of a multicomponent receptor for GDNF."
 RL Nature 382:80-83(1996).
 CC -1- FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED
 CC AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR.
 CC WITH THE DISULFIDE-LINKED GDNF DIMER AND WITH 2 MOLECULES OF RET.
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER, BRAIN AND KIDNEY.
 CC -1- SIMILARITY: BELONGS TO THE GDNF FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL: U59486; AAC52663.1; -
 DR EMBL: U97142; AAC53300.1; -
 KW Receptor; Glycoprotein; GPI-anchor; Membrane; signal.
 FT SIGNAL 1 24
 FT CHAIN 25 430 GDNF RECEPTOR ALPHA.
 FT PROPEP 431 468 HYDROPHOBIC, REMOVED DURING MATURATION
 FT (POTENTIAL).
 FT DOMAIN 362 369 POLY-THR.
 FT CARBOHYD 359 359 POTENTIAL.
 FT CARBOHYD 347 347 POTENTIAL.
 FT CARBOHYD 406 406 POTENTIAL.
 FT LIPID 430 430 GPI-ANCHOR (POTENTIAL).
 SO SEQUENCE 468 AA; 51649 MW; 6A7A2B2A CRC32;

Query Match 23.9%; Score 483.5; DB 1; Length 468;
 Best Local Similarity 34.2%; Pred. No. 7.1e-33;
 Matches 121; Conservative 40; Mismatches 124; Indels 69; Gaps 11;

17 LLLPLPSPPLAAGDPLPESRLMNSCLARRKCAQDPGSAAYHHLDSCS---70

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Db 6 LYPALPLDLLMSVSGDRL-----DCVNASDOCLKEGSCSTKRYTLROCVAGKE 57
Qy 70 ---SISTPLPSEPSVPADCLEAAOQLRNSLIGCMCHRRKNOVACLDIYVTHA----- 122
Db 58 TNSLSLGSLEAKD-----EERSAMEALKOKSLYNCRCRKKKCKKNCCLRIYMSYOSLOG 112
Qy 122 -----PARSLSDL-----CLNFAMLCITLNDKCDRLRK 149
Db 113 NDLEDSPEYEPVNSRLSDIFRAVFIIDVFOQVEHISKGNNCIDAAKACNLDDICKYRS 172
Qy 150 AYGEAC-----SGHCHQRHVCRLRLTFEKAEPHAGLLCPCAPNDGCGERRNTIA 205
Db 173 AATTPCTSVSNDVNCRRCKHKLROFFDKVPARKSHYGMJFCSC--RDIACETERROTIV 230
Qy 206 PNCALPP-VAPNCLTELRLCFSDPLCRSLVDFOHCHPMD-ILGTCAEQ-SRCLRAYL 262
Db 231 PVSYSERERPNCL-LQDSCKTYICRSRLADFTTNCOPESRSVSCLEKNYADCLAYS 290
Qy 263 GLIGTAMTPNVSNTSVALSCTCRSGNLOECEMLEGFFSHNPLCTEATAIA 316
Db 291 GLIGTAMTPNVSNTSVALSCTCRSGNLOECEMLEGFFSHNPLCTEATAIA 344

RESULT 7
GDNF_HUMAN
ID GDNF_HUMAN STANDARD; PRT; 464 AA.
AC P56159;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE GDNF RECEPTOR ALPHA PRECURSOR (GDNF-ALPHA) (TGF-BETA RELATED
DE NEUROTROPHIC FACTOR RECEPTOR 1).
GN GFRAL OR GDNFRA OR TRNRI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP TISSUE-SUBSTANTIA NIGRA;
RX MEDLINE; 96270513.
RA JUNG S., WEN D., YU T., HOUST P.L., LIO Y., FANG M., TAMIR R.,
RA ANTONIO L., HU Z., CUPPLES R., LOUIS J.-C., HU S., ALFRECK B.W.,
RA FOX-G.M.;
RA "GDNF-induced activation of the ret protein tyrosine kinase is
RA mediated by GDNF-alpha, a novel receptor for GDNF.";
RA Cell 85:1113-1124(1996).
RN [2]
RP FUNCTION: RECEPTOR FOR GDNF. MEDIATES THE GDNF-INDUCED
RP AUTOPHOSPHORYLATION AND ACTIVATION OF THE RET RECEPTOR (BY
RP SIMILARITY).
CC -1- SUBUNIT: 2 MOLECULES OF GDNF-ALPHA ARE THOUGHT TO FORM A COMPLEX
CC WITH THE DISULFIDE-LINKED GDNF DIMER AND 2 MOLECULES OF RET (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE GDNF FAMILY.
DR MIM: 601496;
DR Receptor; Glycoprotein; GPI-anchor; Membrane; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 428 GDNF RECEPTOR ALPHA.
FT PROPEP 429 464 HYDROPHOBIC, REMOVED DURING MATURATION
FT (POTENTIAL).
FT DOMAIN 361 368 POLY-THR.
FT CARBOHYD 59 59 POTENTIAL.
FT CARBOHYD 346 346 POTENTIAL.
FT CARBOHYD 405 405 POTENTIAL.
FT LIPID 428 428 GPI-ANCHOR (POTENTIAL).
SQ SEQUENCE 464 AA; 51291 MW; 2C8C3574 CRC32;
Query Match 23.5%; Score 475; DB 1; Length 464;
Best Local Similarity 34.2%; Pred. No. 3.5e-32;
Matches 121; Conservative 42; Mismatches 121; Indels 70; Gaps 12;

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Qy 17 LLLPLPSPPLPLA-----GDPPLTESLIMNSCLARRKQADPTCSAAHHLDSCS---- 70
Db 6 LYPALPLDLLMSVSGDRL-----DCVNASDOCLKEGSCSTKRYTLROCVAGKE 57
Qy 70 ---SISTPLPSEPSVPADCLEAAOQLRNSLIGCMCHRRKNOVACLDIYVTHA----- 124
Db 58 TNSLSLGSLEAKD-----EERSAMEALKOKSLYNCRCRKKKCKKNCCLRIYMSYOSLOG 112
Qy 124 -----RSLSDL-----CLNFAMLCITLNDKCDRLRK 149
Db 113 NDLEDSPEYEPVNSRLSDIFRAVFIIDVFOQVEHISKGNNCIDAAKACNLDDICKYRS 172
Qy 150 AYGEAC-----SGHCHQRHVCRLRLTFEKAEPHAGLLCPCAPNDGCGERRNTIA 205
Db 173 AATTPCTSVSNDVNCRRCKHKLROFFDKVPARKSHYGMJFCSC--RDIACETERROTIV 230
Qy 206 PNCALPP-VAPNCLTELRLCFSDPLCRSLVDFOHCHPMD-ILGTCAEQ-SRCLRAYL 262
Db 231 PVSYSERERPNCL-LQDSCKTYICRSRLADFTTNCOPESRSVSCLEKNYADCLAYS 289
Qy 263 GLIGTAMTPNVSNTSVALSCTCRSGNLOECEMLEGFFSHNPLCTEATAIA 316
Db 290 GLIGTAMTPNVSNTSVALSCTCRSGNLOECEMLEGFFSHNPLCTEATAIA 343

RESULT 8
NOTC_DROME
ID NOTC_DROME STANDARD; PRT; 2703 AA.
AC P07207; P04154;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE NEUROGENIC LOCUS NOTCH PROTEIN PRECURSOR.
GN N.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86079539.
RA WHARTON K.A., JOHANSEN K.M., XU T., ARTAVANIS-TSAKONAS S.;
RT "Nucleotide sequence from the neurogenic locus notch implies a gene
RT product that shares homology with proteins containing EGF-like
RT repeats.";
RT Cell 43:567-581(1985).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-OREGON-R;
RX MEDLINE; 87064624.
RA KIDDO S., KELLEY M.R., YOUNG M.W.;
RT "Sequence of the notch locus of Drosophila melanogaster: relationship
RT of the encoded protein to mammalian clotting and growth factors.";
RL Mol. Cell. Biol. 6:3094-3108(1986).
RN [3]
RP SEQUENCE OF 2505-2611 FROM N.A.
RX MEDLINE; 85099329.
RA WHARTON K.A., YEDVOBNICK B., FINNERTY V.G., ARTAVANIS-TSAKONAS S.;
RT "ope: a novel family of transcribed repeats shared by the Notch locus
RT and other developmentally regulated loci in D. melanogaster.";
RL Cell 40:55-62(1985).
RN [4]
RP SEQUENCE OF 1-8 FROM N.A.
RX MEDLINE; 87257846.
RA KELLEY M.R., KIDDO S., BERG R.L., YOUNG M.W.;
RT "Restriction of P-element insertions at the Notch locus of Drosophila
RT melanogaster.";
RL Mol. Cell. Biol. 7:1545-1548(1987).
RN [5]
RP REVIEW.
RA HARRIS W.A.;
RT "Many cell types specified by Notch function.";

```


1	2400	51.3	884	4	014953	014953 homo sapien
2	2337.5	50.0	723	4	012787	012787 homo sapien
3	2246	48.0	876	11	060752	060752 mus musculus
4	2080	44.5	856	11	062131	062131 mus musculus
5	1888	40.4	397	11	055243	055243 mus musculus
6	1888	40.4	397	11	035335	035335 mus musculus
7	1880	40.2	397	11	035118	035118 mus musculus
8	1728.5	37.0	873	13	098949	098949 gallus gallus
9	1564	33.5	400	4	060609	060609 homo sapien
10	1257	27.7	874	13	093166	093166 brachydanio
11	1153.5	24.7	999	4	012866	012866 homo sapien
12	1146	24.5	511	11	062134	062134 mus musculus
13	1137	24.3	994	11	060805	060805 mus musculus
14	1102.5	23.6	974	13	090777	090777 gallus gallus
15	81.1	17.3	600	4	045516	045516 homo sapien
16	697	14.9	1369	13	P79950	P79950 xenopus laevis
17	696	14.9	1369	13	P70003	P70003 xenopus laevis
18	678	14.5	1374	13	093600	093600 fugu rubripes
19	668.5	14.3	570	5	097191	097191 geodia cydotea
20	662.5	14.2	596	12	085448	085448 avian carci
21	659.5	14.1	1375	13	093605	093605 fugu rubripes
22	658.5	14.1	1404	13	062190	062190 mus musculus
23	645.5	13.8	1378	11	062355	062355 mus musculus
24	645.5	13.8	1378	11	062355	062355 mus musculus
25	617.5	13.2	1382	13	090915	090915 gallus gallus
26	615	13.2	1425	13	093607	093607 fugu rubripes
27	609	13.0	1382	11	P97579	P97579 rattus norvegicus
28	609	12.9	455	4	042875	042875 homo sapien
29	602	12.9	2554	5	024512	024512 drosophila

30	600	12.8	1373	11	070438	070438 mus musculus
31	597	12.8	1382	11	P97523	P97523 rattus norv
32	588.5	12.6	609	13	Q91776	Q91776 xenopus lae
33	586	12.5	464	11	035977	035977 rattus norv
34	585	12.5	899	4	003962	003962 homo sapien
35	582.5	12.5	1418	13	093457	093457 pssetta max
36	582	12.4	464	4	015316	015316 homo sapien
37	582	12.4	464	4	015338	015338 homo sapien
38	579.5	12.4	1358	13	073798	073798 xenopus lae
39	579.5	12.4	1064	13	090601	090601 gallus gall
40	578.5	12.4	1106	13	P79726	P79726 brachydanid
41	577	12.3	1106	13	042362	042362 brachydanid
42	574	12.3	476	13	073845	073845 oncorhynch
43	570.5	12.2	981	12	039477	039477 abelison mur
44	570.5	12.2	980	12	092809	092809 abelison mur
45	570.5	12.2	1245	13	Q9YH8	Q9YH8 pssetta maxi

ALIGNMENTS

```

RESULT 1
014953
ID 014953 PRELIMINARY; PRT; 884 AA.
AC 014953;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE PROTEIN-TYROSINE KINASE.
GN BYR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN.
RX MEDLINE; 97318332.
RA KATU Y., NINOMIYA D., KATO M., MIZUGUCHI M., SAJI M., KATSUMOTO T.,
RA OHNO K., TAKASHIMA S., ONODERA K.;
RT "A tyrosine kinase-like molecule is localized in the nuclear membrane
RT of neurons: hippocampal behavior under stress.";
RL Biol. Cell 88:45-54(1996).
DR EMBL; D50479; BAA21781.1;
DR PFAM; PF00041; fn3. 2.
DR PFAM; PF00047; 1g. 2.
DR PFAM; PF00069; pkinase. 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW Tyrosine-protein kinase.
SO SEQUENCE 884 AA; 96179 MW; 624CD0A9 CRC32;

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Query Match	Score	DB 4	Length
51.3%	2400	884	
Best Local Similarity	95.8%	7 00-10	

Matches	466;	Conservative	5;	Mismatches	15;	Indels	0;	Gaps	0
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QY	382	QSDMADUSFESVVOOQNSNPRKAWPVVTGVTALTATYAAALAILLRKRETRFGOAF	444
	399	WSOPLYVSHDRAGQGGPHSRSTWVWVYGVJTAATYAAALAILLRKRETRFGOAF	458
QY	442	DSVMANGEPAAVFFRAARSFNRRPERFEATLDSIGSIDELKREKEDVYIIPROOFTLRML	502
Db	459	DSVMANGEPAAVFFRAARSFNRRPERFEATLDSIGSIDELKREKEDVYIIPROOFTLRML	518
QY	502	GGGERSVREAOLOKODGSFYKVAVKYKLTADITASSDIEEFLREAAKKEFDHPHVARLY	561
Db	519	GGGERSVREAOLOKODGSFYKVAVKYKLTADITASSDIEEFLREAAKKEFDHPHVARLY	578
QY	562	GVSLNSRAKAGLPIPMVYLFPMKGGDHAFLASRGENPFLPLOTILRPMNDIAGME	621
Db	579	GVSLNSRAKAGLPIPMVYLFPMKGGDHAFLASRGENPFLPLOTILRPMNDIAGME	638
QY	622	YLSRRKFIHRDLAARNCMLEADNTVCVADFGSLRKYTSGDYIROGCAKSLPVKWTALESTL	681

	723 AA.	PRT;	PRELIMINARY;	723 AA.	1/87	2
AC	012787;					
AD	01-NOV-1996 (Tremblrel, 01, Created)					
DT	01-NOV-1996 (Tremblrel, 01, last sequence update)					
DT	01-MAY-1999 (Tremblrel, 10, last annotation update)					
DE	RECEPTOR TYROSINE KINASE (FRAGMENT).					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Crnata; Vertebrata; Mammalia;					
OC	Eutheria; Primates; Catarrhini; Homiidae; Homo.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE; 94151024.					
RA	DAI W., PAN H., HAMDY H., GUPTA S.L., MURPHY M.J.;					
RT	"Molecular cloning of a novel receptor tyrosine kinase, tlf, highly expressed in human ovary and testis."					
RL	Oncogene 9:975-979(1994).					
DR	EMBL: U02566; AAA17407.1;					
DR	PFAM: PF00041; fn3; 2.					
DR	PFAM: PF00069; pkinase; 1.					
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.					
DR	PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.					
FT	NON TER					
SO	SEQUENCE					
	723 AA; 78787 MW; B667D834 CRC32;					

RESULT 3

ID 060752 PRELIMINARY: PR: 8/6 AA.

AC 060752; 009080; 062482; P70285; 009070;

DT 01-NOV-1996 (TReMBLeI. 01, Created)

DT 01-NOV-1996 (TReMBLeI. 01, Last sequence update)

DT 01-MAY-1999 (TReMBLeI. 10, Last annotation update)

DE TYRO3 PROTEIN TYROSINE KINASE 3

DE (PUTATIVE GROWTH FACTOR RECEPTOR TYROSINE KINASE B) (TYRO3)

DE (TYROSINE KINASE GROWTH FACTOR RECEPTOR ISOFORM 1) (FRAGMENT).

GN TYRO3 OR ETK2/TYRO3.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

[1]

RP SEQUENCE FROM N.A.

RC STRAIN-BALB/C; TISSUE-BRAIN;

RA MEDLINE; 95240399.

RX SCHULTZ N., PAULHAC C., LEE L., ZHOU R.;

RT "Isolation and expression analysis of tyro3, a murine growth factor

RL receptor tyrosine kinase preferentially expressed in adult brain.";

RL Mol. Brain Res. 28:273-280(1995).

[2]

RP SEQUENCE FROM N.A.

RC STRAIN-BALB/C; TISSUE-BRAIN;

RA MEDLINE; 94193774.

RX MARK M.R., SCADDEN D.T., WANG Z., GU Q., GODDARD A., GODOWSKI P.T.;

RT "Tse, a novel receptor-type tyrosine kinase with homology to Axl/Ufo,

RL is expressed at high levels in the brain.";

RL J. Biol. Chem. 269:10720-10728(1994).

[3]

RP SEQUENCE FROM N.A.

RC STRAIN-BALB/C; TISSUE-BRAIN;

RA MEDLINE; 94150990.

RX FUJIMOTO J., YAMAMOTO T.;

RT "prt, a mouse gene encoding a novel receptor-type protein-tyrosine

RL kinase, is preferentially expressed in the brain.";

RL Oncogene 9:693-698(1994).

[4]

RP SEQUENCE FROM N.A.

RC STRAIN-BALB/C; TISSUE-BRAIN;

RA MEDLINE; 97044738.

RX SASAKI M., ENAMI J.;

RT "Structure and expression of a murine homologue of sky receptor

RL tyrosine kinase gene.";

RL J. Biochem. 120:264-270(1996).

[5]

RP SEQUENCE OF 1-88 FROM N.A.

RC STRAIN-129SV; TISSUE-LIVER;

RA MEDLINE; 95303687.

RX BIESCHKEK L.G., GIANNOLA D.M., EMERSON S.G.;

RT "Identification of alternative exons, including a novel exon, in the

RL tyrosine kinase receptor gene Etk2/tyro3 that explain differences in

RL 5' CDNA sequences.";

RL Oncogene 10:2239-2242(1995).

[6]

RP SEQUENCE FROM N.A.

RC STRAIN-BALB/C; TISSUE-BRAIN;

2X MEDLINE: 94150991.
 2A OHASHI K., MIZUNO K., KUMA K., MIYATA T., NAKAMURA T.;
 2T Cloning of the cDNA for a novel receptor tyrosine kinase, Sky,
 2T predominantly expressed in brain.";
 2L Oncogene 9:699-705(1994).
 2N [1]

3P SEQUENCE FROM N.A.

3C STRAIN-BALB/C;

3A SASAKI M.;

3L Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.

3R EMBL: AB000826; BAA19191.1; -

3R EMBL: AB000827; BAA19192.1; -

3R EMBL: U18343; AAB26943.1; -

3R EMBL: U23721; AAC52215.1; -

3R EMBL: U23718; AAC52215.1; JOINED.

3R MGI: 104294; TYRO3.

3R PFAM: PF00041; fn3; 2.

3R PFAM: PF00047; 1g; 2.

3R PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.

3R PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.

3R NON_TER 876 876

3R SEQUENCE 876 AA; 96055 MW; 54D682DB CRC32;

Query Match 48.0%; Score 2246; DB 11; Length 876;

Best Local Similarity 90.1%; Pred. No. 7,6e-181;

Matches 438; Conservative 14; Mismatches 34; Indels 0; Gaps 0;

382 FSDMDSTFVSVOQNSNPANRAMPVVLGVLTALVTAAALILRRKRETRFGQAF 441

391 WSQPLVSSHHDHAGRGPPHSRTSWPVVLGVLTALVTAAALILRRKRETRFGQAF 450

442 DSYMAGEPAVHFRARSRNRRPERIEATLDSIGISDELKELDEVLIPEQOFTLGRML 501

451 DSYMAGEPAVHFRARSRNRRPERIEATLDSIGISDELKELDEVLIPEQOFTLGRML 510

502 GGEFGSVREAOLOKODGSFVAVKMLKADIIASSDIEFLREAAKKEFDHPYAKLY 561

511 GGEFGSVREAOLOKODGSFVAVKMLKADIIASSDIEFLREAAKKEFDHPYAKLY 570

562 GVSLSRAAGRLPIPVYIIPFKHGDHLAFLASRIGENFNLPLQTLIRFVNDIACGNE 621

574 GVSLSRAAGRLPIPVYIIPFKHGDHLAFLASRIGENFNLPLQTLIRFVNDIACGNE 630

622 YSSSRFTIRDLAARNCMAEDMTVCVADFGLSRKYSGDYRQGCASKLPMKWTALDSL 681

631 YSSSRFTIRDLAARNCMAEDMTVCVADFGLSRKYSGDYRQGCASKLPMKWTALDSL 690

682 ADNLTYVSDVNAFVGTWMEIMTRGOTPYAGIENAEIYNYLIGGNRLKOPPECMEDVYDL 741

691 ADNLTYVSDVNAFVGTWMEIMTRGOTPYAGIENAEIYNYLIGGNRLKOPPECMEDVYDL 750

742 MYQCSADPKQPSFTCLMELENILIGOLSVLASODPLYINIERAEPTAGSLELPER 801

751 MYQCSADPKQPSFTCLMELENILIGOLSVLASODPLYINIERAEPTAGSLELPER 810

802 DOPYSGADDSGSMGAVGTPSDCRITLITGGIAGLAPGQAEHPESPFLNTQRLLLQGL 861

811 ERSSSEADGDSGAVGTPSDCRITLITGGIAGLAPGQAEHPESPFLNTQRLLLQGL 870

862 LPHSSC 867

871 LPHSSC 876

RESULT 4 PRELIMINARY; PRT; 856 AA.

ID 062121

AC 062121;

DT 01-NOV-1996 (Tremblrel. 01, Created)

DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)

DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)

DE PROTEIN TYROSINE KINASE.

OS Mus musculus (mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-BRAIN;

RX MEDLINE: 94150990.

RA FUJIMOTO J., YAMAMOTO T.;

RT Drl, a mouse gene encoding a novel receptor-type protein-tyrosine

RT kinase, is preferentially expressed in the brain.";

RL Oncogene 9:693-698(1994)

DR EMBL: D17393; BAA04216.1; -

DR MGI: 104294; TYRO3.

DR PFAM: PF00041; fn3; 2.

DR PFAM: PF00047; 1g; 2.

DR PFAM: PF00069; PKinase; 1.

DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.

DR SEQUENCE 856 AA; 93930 MW; 2DEBFC84 CRC32;

Query Match 44.5%; Score 2080; DB 11; Length 856;

Best Local Similarity 87.7%; Pred. No. 7,4e-167;

Matches 408; Conservative 15; Mismatches 40; Indels 2; Gaps 1;

382 FSDMDSTFVSVOQNSNPANRAMPVVLGVLTALVTAAALILRRKRETRFGQAF 441

390 WSQPLVSSHHDHAGRGPPHSRTSWPVVLGVLTALVTAAALILRRKRETRFGQAF 449

442 DSYMAGEPAVHFRARSRNRRPERIEATLDSIGISDELKELDEVLIPEQOFTLGRML 501

450 DSYMAGEPAVHFRARSRNRRPERIEATLDSIGISDELKELDEVLIPEQOFTLGRML 509

502 GGEFGSVREAOLOKODGSFVAVKMLKADIIASSDIEFLREAAKKEFDHPYAKLY 561

510 GGEFGSVREAOLOKODGSFVAVKMLKADIIASSDIEFLREAAKKEFDHPYAKLY 569

562 GVSLSRAAGRLPIPVYIIPFKHGDHLAFLASRIGENFNLPLQTLIRFVNDIACGNE 621

570 GVSLSRAAGRLPIPVYIIPFKHGDHLAFLASRIGENFNLPLQTLIRFVNDIACGNE 629

622 YSSSRFTIRDLAARNCMAEDMTVCVADFGLSRKYSGDYRQGCASKLPMKWTALDSL 681

630 YSSSRFTIRDLAARNCMAEDMTVCVADFGLSRKYSGDYRQGCASKLPMKWTALDSL 689

682 ADNLTYVSDVNAFVGTWMEIMTRGOTPYAGIENAEIYNYLIGGNRLKOPPECMEDVYDL 741

690 ADNLTYVSDVNAFVGTWMEIMTRGOTPYAGIENAEIYNYLIGGNRLKOPPECMEDVYDL 749

742 MYQCSADPKQPSFTCLMELENILIGOLSVLASODPLYINIERAEPTAGSLELPER 801

750 MYQCSADPKQPSFTCLMELENILIGOLSVLASODPLYINIERAEPTAGSLELPER 809

802 DOPYSGADDSGSMGAVGTPSDCRITLITGGIAGLAPGQAEHPESPFLNTQRLLLQGL 844

810 ERSSSEADGDSGAVGTPSDCRITLITGGIAGLAPGQAEHPESPFLNTQRLLLQGL 854

854

RESULT 5 PRELIMINARY; PRT; 397 AA.

ID 055243

AC 055243;

DT 01-JUN-1998 (Tremblrel. 06, Created)

DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)

DT 01-JUN-1998 (Tremblrel. 06, Last annotation update)

DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR FAMILY RECEPTOR ALPHA-3.

GN GFR3.

OS Mus musculus (mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RN [1]

RP SEQUENCE FROM N.A.

RA WIDENFALK J., TOMAC A., LINDOVIST E., HOFER B., OLSON L.,
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA NAVEILHAN P., BAUDET C., MIKAELS O., SHEN L., WESTPHAL H.,
 RA ERNFORS P.,
 RA Proc. Natl. Acad. Sci. U.S.A. 0:0-0(1997).
 DR EMBL; AF041842; AAC23558.1;
 DR EMBL; AF036163; AAC24468.1;
 SQ SEQUENCE 397 AA; 44302 MW; F77607CF CRC32;

Query Match 40.4%; Score 1888; DB 11; Length 397;
 Best Local Similarity 94.4%; Pred. No. 3.7e-151;
 Matches 355; Conservative 5; Mismatches 10; Indels 6; Gaps 1;

QY 54 LEAGNSLATENRFVNSCTOARKKCEANPACAAVOHLGSCSTSLRPLPLESAMSADCL 113
 DB 25 LGAGNSLATENRFVNSCTOARKKCEANPACAAVOHLGSCSTSLRPLPLESAMSADCL 84
 DB 114 EAAEQLRNSSLIDCRCHRRKHOATCLDIYTWHPARSLGDELDVSPYEDVTYSKPKM 173
 DB 85 EAAEQLRNSSLIDCRCHRRKHOATCLDIYTWHPARSLGDELDVSPYEDVTYSKPKM 144
 QY 174 NLSKLNMLKPDSDCLKFAMLCTLHDKCDRLKRAYGAGSGIRORHLCLAOISFEKA 233
 DB 145 NLSKLNMLKPDSDCLKFAMLCTLHDKCDRLKRAYGAGSGIRORHLCLAOISFEKA 204
 QY 234 AESHAQGLLCCPCPEDAGCGERRNTIAPSCALPSTVPCNCLDRSFCRADPLCRSLMD 293
 DB 205 AESHAQGLLCCPCPEDAGCGERRNTIAPSCALPSTVPCNCLDRSFCRADPLCRSLMD 264
 QY 294 FQTHCHPMIILGTCATEOSRCIRAYLIGLIGTANTPNFISKVNTVAALSCGSGNLODE 353
 DB 265 FQTHCHPMIILGTCATEOSRCIRAYLIGLIGTANTPNFISKVNTVAALSCGSGNLODE 324
 QY 354 CEOLERSFSONPCLVEALAAKRFHROLFSQDMADSTSVYQOONSNAWAPVVLGV 413
 DB 325 CEOLERSFSONPCLVEALAAKRFHROLFSQDMADSTSVYQOONSNAWAPVVLGV 378
 QY 414 LTALVTAALALILR 429
 DB 379 RLPIISFILPILILQ 394
 RESULT 6
 ID 035325 PRELIMINARY; PRT: 397 AA.
 035325;
 01-JAN-1998 (TREMblrel. 05, Created)
 01-JAN-1998 (TREMblrel. 05, Last sequence update)
 01-AUG-1998 (TREMblrel. 07, Last annotation update)
 DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR FAMILY RECEPTOR ALPHA-3.
 GN GFR-3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TROPP M., RAYNOSCHER C., IBANEZ C.F.,
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF020305; AAB70931.1;
 SQ SEQUENCE 397 AA; 44333 MW; F0C0C841 CRC32;

Query Match 40.4%; Score 1888; DB 11; Length 397;
 Best Local Similarity 94.4%; Pred. No. 3.7e-151;
 Matches 355; Conservative 5; Mismatches 10; Indels 6; Gaps 1;
 QY 54 LEAGNSLATENRFVNSCTOARKKCEANPACAAVOHLGSCSTSLRPLPLESAMSADCL 113
 DB 25 LGAGNSLATENRFVNSCTOARKKCEANPACAAVOHLGSCSTSLRPLPLESAMSADCL 84

QY 114 EAAEQLRNSSLIDCRCHRRKHOATCLDIYTWHPARSLGDELDVSPYEDVTYSKPKM 173
 DB 85 EAAEQLRNSSLIDCRCHRRKHOATCLDIYTWHPARSLGDELDVSPYEDVTYSKPKM 144
 QY 174 NLSKLNMLKPDSDCLKFAMLCTLHDKCDRLKRAYGAGSGIRORHLCLAOISFEKA 233
 DB 145 NLSKLNMLKPDSDCLKFAMLCTLHDKCDRLKRAYGAGSGIRORHLCLAOISFEKA 204
 QY 234 AESHAQGLLCCPCPEDAGCGERRNTIAPSCALPSTVPCNCLDRSFCRADPLCRSLMD 293
 DB 205 AESHAQGLLCCPCPEDAGCGERRNTIAPSCALPSTVPCNCLDRSFCRADPLCRSLMD 264
 QY 294 FQTHCHPMIILGTCATEOSRCIRAYLIGLIGTANTPNFISKVNTVAALSCGSGNLODE 353
 DB 265 FQTHCHPMIILGTCATEOSRCIRAYLIGLIGTANTPNFISKVNTVAALSCGSGNLODE 324
 QY 354 CEOLERSFSONPCLVEALAAKRFHROLFSQDMADSTSVYQOONSNAWAPVVLGV 413
 DB 325 CEOLERSFSONPCLVEALAAKRFHROLFSQDMADSTSVYQOONSNAWAPVVLGV 378
 QY 414 LTALVTAALALILR 429
 DB 379 RLPIISFILPILILQ 394
 RESULT 7
 ID 035118 PRELIMINARY; PRT: 397 AA.
 035118;
 01-JAN-1998 (TREMblrel. 05, Created)
 01-JAN-1998 (TREMblrel. 05, Last sequence update)
 01-NOV-1998 (TREMblrel. 08, Last annotation update)
 DE GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR FAMILY RECEPTOR ALPHA 3
 GN GFR3 OR GFRALPHA-3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL6; TISSUE-HEART;
 RX MEDLINE: 98205811.
 RA NAKANO S., ITO S., YANG L.-X., KUCHI K.,
 RT "Molecular cloning and expression analysis of GFR alpha-3, a novel
 RT cDNA related to GDNF alpha and NTR alpha."
 RL Biochem. Biophys. Res. Commun. 244:849-853(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA BALOH R.H., GORODINSKY A., GOLDEN J.P., TANSEY M.G., KECK C.L.,
 RA POBESCU N.C., JOHNSON E.M. JR., MILBRANDT J.,
 RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(1998).
 DR EMBL; AF008833; BAA23562.1;
 DR EMBL; AF051766; AAC24354.1;
 DR MDL; MG1:1201403; GFR3.
 SQ SEQUENCE 397 AA; 44307 MW; A80E0D24 CRC32;

Query Match 40.2%; Score 1880; DB 11; Length 397;
 Best Local Similarity 94.1%; Pred. No. 1.7e-150;
 Matches 354; Conservative 5; Mismatches 11; Indels 6; Gaps 1;
 QY 54 LEAGNSLATENRFVNSCTOARKKCEANPACAAVOHLGSCSTSLRPLPLESAMSADCL 113
 DB 25 LGAGNSLATENRFVNSCTOARKKCEANPACAAVOHLGSCSTSLRPLPLESAMSADCL 84
 QY 114 EAAEQLRNSSLIDCRCHRRKHOATCLDIYTWHPARSLGDELDVSPYEDVTYSKPKM 173
 DB 85 EAAEQLRNSSLIDCRCHRRKHOATCLDIYTWHPARSLGDELDVSPYEDVTYSKPKM 144
 QY 174 NLSKLNMLKPDSDCLKFAMLCTLHDKCDRLKRAYGAGSGIRORHLCLAOISFEKA 233
 DB 145 NLSKLNMLKPDSDCLKFAMLCTLHDKCDRLKRAYGAGSGIRORHLCLAOISFEKA 204

[illegible]

Query Match	33.5%	Score 1564;	DB 4;	Length 400;
Best Local Similarity	75.8%	Pred. No. 8e-124;		
Matches 291;	Conservative 27;	Mismatches 56;	Indels 10;	Gaps 2;

QY	47	LPVLDQLLENGNSL	ATENFVNSCTQARRKCEANPACAAAYOHLSGCTSSLSRPL	LEES	106
DB	21	LPSPPLPLAAGPLP	PESHRLMNSCLQARRKCOADPTCSAAVHHNDSCTSSIS	TPLPSEEP	80
QY	107	AMASADCEAAEOLR	NSLIDRCRCHRMKHOATCDIWTYTPARSLGDELDVSP	EDTV	166
DB	81	SVAPDCLLEAAGLR	NSSLIGCCCHRRMKNOVACDITWTYHRASLDENYLDVSP	EDTV	140
QY	167	TSPRPMKMTSKT	NMLKPSDCLCFKFAWLCILDHRCDRIRKAYGACSGIRG	QHRLCIAOL	226
DB	141	TSPRPMKMTSKT	NMLKPSDCLCFKFAWLCILDHRCDRIRKAYGACSGIRG	QHRLCIAOL	200
QY	227	RSPFEKAASHNOGL	LICPCPPEDAGCGERRRNTIAPSCALPSTYPPCCLDRSFC	ADPL	286
DB	201	LTFEEPAAPRHAG	LGLLPCAPANDGCGERRRNTIAPSCALPVPAPPCCLDR	IRLRCFSDPL	260
QY	287	CRSLRMDFO	THCPMDILGTCAEQSRCLRAIYLIGLSTATPNEISKVTNTVAL	STCGRG	346
DB	261	CRSLRMDFO	THCPMDILGTCAEQSRCLRAIYLIGLSTATPNEISKVTNTVAL	STCGRG	320
QY	347	SGMLDCECQLR	SRSSQNPCLVEALIAAMRHRQLFSQDMAADSTFSYVOQ	ONSPPAMR--	405
DB	321	SGMLDCECQLR	SRSSQNPCLVEALIAAMRHRQLFSQDMAADSTFSYVOQ	ONSPPAMR	380
QY	405	AAMPVAVIGV	LTALTAALATLIL	428	
DB	381	PWPVSLF-----	SCTLPLILL	396	

RESULT	10
QY	09Y166
ID	09Y166
AC	09Y166;
DT	01-MAY-1999 (TREMBLrel. 10, Created)
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT	01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE	DEVELOPMENTAL RECEPTOR TYROSINE KINASE.
EN	DTK.

	PRELIMINARY;	PRT;	874 AA.
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OS Brachydanio rerio (zebrafish) (zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
 OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Cyprinidae; Rasbora; Danio.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA WALSH J.A., JANSZ-PEREZ M., CROSIER K.E., EVANS C.W., CROSIER P.S.;
 RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF021344; AAD01694.1;
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 KW Receptor; Kinase.
 SO SEQUENCE 874 AA; 97599 MW; 17DC56DD CRC32;

Query Match 27.7%; Score 1297; DB 13; Length 874;
 Best Local Similarity 51.8%; Pred. No. 8.5e-101;
 Matches 287; Conservative 73; Mismatches 140; Indels 54; Gaps 13;

348 GNLDECEBOLERSF-----SONPCLVEAIAAK-----RFRHOLF----- 383
 329 GRQGEELRGRRLAYKLQWNGGSEODPLLFKEVNAHLSGAGFFNATFOVAACMGCGP 388
 383 -SODMADSTFVYVQOONSPPANRAWVPVULGVTALVTAALAILLRKRKTRFGQAF 441
 389 WSPQVYVMSVMAQOTQR--GMMWGLLGLVATM-VGLLLVLRNKGKTFQGSF 445
 442 DSVYARG-EPAYHFAARSFNRPERIEATLDSIGISDELKEKEDVLIIPQOFLGSM 500
 446 ---AAGGAVPVSFTNARFNNQFPELPSTDSIGINDLAKDLVILFERLLTLGRM 502
 501 LGKGEVSREAOIKOEDGSFVKAVAKMLKADIIASSDIEELREAAKKEEDHPHVA 560
 503 LGGEGSVREAFLEKSENNSGQKVAVKLKTIDINSSDIEQCKEAAVKKDPHHPV 562
 561 VGVLSRKAQRPLPIMVILPFMKHGDHLAFILASRIGENPNPLQTLIRKWDIAGM 620
 563 IGVSLHRAQOQLPIMVILPFMKHGDHLFTLMSRLGEPFTSQOILIOFMLIARGM 622
 621 EYLSRNFTHRDLAARNCLMADMTVCVADFGLSRKYSGDYRQGCASKLPVKMLAES 680
 623 EYLSRNFTHRDLAARNCLMADMTVCVADFGLSRKYSGDYRQGCASKLPVKMLAES 682
 681 LADNYTQSDVWAFGVTWMTMTGQTPYAGIEENAEIYNIILGKRLKQPECEMED 740
 683 LADNYTQSDVWAFGVTWMTMTGQTPYAGIEENAEIYNIILGKRLKQPECEMED 742
 741 LMYQCSADPKORPSFTCLMELENIIGQSLYSASQDPLYNIR--AEETAG-GSLE 797
 743 IMHSCSPVKCRPSFOHLIDOLELMAKLNAPYKEPLLVLNLEEDGEGQANSSTRSE 802
 798 LGRDQPYSGAG-----DQSGMAGVGTSPDCRYILTP--GGLAEPQCAHEQ 843
 803 EPMWGVPMQCAIEDEKMDLWVSSGAL-AIGG---DYRIITIGSVNAIDESHSE 858
 844 PESPINTEORLL 857
 859 LSEDIREEEDVIT 872

RESULT 11

012866 PRELIMINARY; PRT; 999 AA.
 AC 012866
 DT 01-NOV-1996 (TRENDArel. 01, Created)
 DT 01-NOV-1996 (TRENDArel. 01, Last sequence update)
 DT 01-AUG-1999 (TRENDArel. 11, Last annotation update)
 DE CELLULAR PROTO-ONCOGENE (C-MER) PRECURSOR (C-MER).
 GN C-MER.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE-PERIPHERAL BLOOD LEUKOCYTES;
 RX MEDLINE; 94368701.
 RA GRAHAM D.K., DAWSON T.L., MULLANEY D.L., SNOODGRASS H.R., EARP H.S.;
 RT "Cloning and mRNA expression analysis of a novel human protooncogene,
 RT Cell Growth Differ. 5:647-657(1994).
 RL [2]
 RN ERRATUM.
 RA GRAHAM D.K., DAWSON T.L., MULLANEY D.L., SNOODGRASS H.R., EARP H.S.;
 RC Cell Growth Differ. 5:1022-1022(1994).
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC THE EXTRACELLULAR DOMAINS CONTAINS 2 IG-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 DR EMBL: U08023; AAB60430.1;
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PFM: PF00041; In3; 2.
 DR PFM: PF00041; In3; 2.
 DR PFM: PF00069; Pkinase; 1.
 KW Proto-oncogene; Transmembrane; Repeat; Immunoglobulin domain; Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 999
 FT DOMAIN 19 501
 FT DOMAIN 90 182
 FT DOMAIN 198 266
 FT DOMAIN 283 372
 FT DOMAIN 376 480
 FT TRANSMEM 502 518
 FT DOMAIN 519 999
 FT CYTOPLASMIC (POTENTIAL).
 SO SEQUENCE 999 AA; 110390 MW; 20274ED6 CRC32;

Query Match 24.7%; Score 1155.5; DB 4; Length 999;
 Best Local Similarity 38.8%; Pred. No. 8.9e-89;
 Matches 294; Conservative 115; Mismatches 207; Indels 141; Gaps 27;

233 AAESH-----AAGLL-----CCPEPDAGGERRRTTAPSCALPV-----TP--N 273
 261 SCEANDKGLVSGQVQINAIISPLEVSI-----NSTHSLIISVWPFQDGYSPRN 316
 274 C-LDIRSCADPLCRSHLMDFTCHCPMDILGTCATQOSCLAY-----LGLIG-TA 325
 317 CSIQVK---EADPLNGSVMIFTSALP---HLQIQQLALNYSIGVSCMNEIGISA 369
 326 MTP-----NFISVNTVAL-----SCTCGS 347
 370 VSPWILASTTEGAPSVAPLNTVFLNLSDDNDVIRWMPKPYKODGELVGRISHVQSA 429
 348 GNLDECEBOLERSFQ-----NPLVEAIAAKMFRHOLF-----QDMAD-S 389
 430 GISELELEEVQONSRRARISVQVNACTVRIAAVTGSGVGFSDPVKIFIPAGWDYA 489
 390 TFSVYVQOONSPPANRAWVPVVLG-----VLTAATAALAILLRKRKTRFGQAF--- 442
 490 PESTPAPGNADP-----VLIFGCGFILLGLIYLSLA---IRKQVEKRFNAFEE 541
 442 DSVYARGEPAYHFAARSFNRPERIEATLDSIGISDELKEKEDVLIIPQOFTLGRM 501
 542 DS-----ELVNYTAKSFRC---RAIETLHSGVSEELONKLEDDVVDNLLILKIL 593
 502 GKGEFVSREAOIKOEDGSFVKAVAKMLKADIIASSDIEELREAAKKEEDHPHVA 561
 594 GEGFEGSVMEGNLKQEGTSLKAVAKMKLNDNSHREIEELSLDAACKDPSHNVIRL 653
 562 GVSLSRAKGRPLPIMVILPFMKHGDHLAFILASRIGENPNPLQTLIRKWDIAGM 621
 654 GVCIEKSSQG-IPRPVILPFMKYGDHLTYLTSRLTGPKHPILOGLLFMDIALGME 712
 622 YLSRNFTHRDLAARNCLMADMTVCVADFGLSRKYSGDYRQGCASKLPVKMLAES 681
 713 YLSRNFTHRDLAARNCLMADMTVCVADFGLSRKYSGDYRQGRYAKMPVKMLAES 772

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QY 682 ANLVVQSDVAAGVYTAIMEIMTRGCTPYVGIENAEYNYLLIGNRLKOPPECEMEDYD 741
Db 11 :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 832
QY 773 ADRVYTSKSDVAAGVYTAIMEIMTRGCTPYVGIENAEYNYLLIGNRLKOPPECEMEDYD 832
Db 11 :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 892
QY 742 MTQCSADRKORPSFTCLRMLEENILGOLSVLSASODPLTN--IERAEPTAGSL-E 797
Db 11 :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 892
QY 833 MYSCWRTDPLDPTFVLRLOLEKLESLPDVANOADVIVYNQULESSGGLAQPTLAP 892
Db 11 :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 892
QY 798 LPGRQPYGAGDGSOMGAVG-----GTPDCRYILTPGG----LAOPGOAEHP 844
Db 11 :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 892
QY 845 EEPINTEORTL-----LLOGLPHSSCADASIKMD 876
Db 11 :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 952
QY 953 KNSVLPGERLVNNGVSWSHSMPLGSSLPDELLEFAD 989
Db 11 :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 952

RESULT 12
62194
062194 PRELIMINARY: PRT: 511 AA.
062194.
01-NOV-1996 (TREMBLrel. 01, Created)
01-NOV-1996 (TREMBLrel. 01, last sequence update)
01-NOV-1998 (TREMBLrel. 08, last annotation update)
RECEPTOR PROTEIN-TYROSINE KINASE (FRAGMENT).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
SEQUENCE FROM N.A.
STRAIN-CD-1; TISSUE-TESTIS;
DOWDS C.A., BURS D.J., SALING P.M.;
Submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.
DR EMBL: L11625; AAA85355.1;
DR PFM: PFM0069; pkinase; 1.
Tyrosine-protein kinase.
NON TER 1
SEQUENCE 511 AA; 57410 MW; 401BIC3A CRC32;

Query Match 24.5%; Score 1146; DB 11; Length 511.
Best Local Similarity 50.2%; Pred. No.2,1e-88;
Matches 246; Conservative 77; Mismatches 121; Indels 46; Gaps 13.

QY 409 VVLG-----VLTALVTAALALILLRKKRRTFQAF--DSYAKGPAVHFRARSF 460
Db 28 IILGCFGFIILGLILCVSLA--LRRVROETKFGAGFSEEDSOL-----VNNYRAKSF 79
461 NRRERERLEATLDSIGIDELKEKEDVLIPDQOTTLKMLCKGEFGSVREAOLOEDGS 520
Db 80 CR--RALELTQSGVSEELONKLEEDVIDNMLVYLGEVGEFGSVREAOLOEDGT 136
QY 521 FVKVAVKMLKADIIASSDIEEFLREAACKKEFDHPVAVLVSVLSRAKGRPLIPMYL 580
Db 137 SQKVAVKMKLDNSQRIIEELSLAACMKDNNHNVIRLGLVCIETLSQG-IIPMYL 195
QY 581 PFKKHGDLHAFLASRIGENPNPLQTLIREVWDIACGMEYLSRNTIHRDLAARNCL 640
Db 196 PFKKHGDLHAFLASRIGENPNPLQTLIREVWDIACGMEYLSRNTIHRDLAARNCL 255
QY 641 AEDMTVCADAGLSKRTISGVYRGGCAKLPYKTLALESADNLYVQSDVMAFGVTMM 700
Db 256 RDMDMVCADAGLSKRTISGVYRGGCAKLPYKTLALESADNLYVQSDVMAFGVTMM 315
QY 701 EIMTRGQTPYVGIENAEYNYLLIGNRLKOPPECEMEDYDLYOCMSADPKORPSFTCLR 760
Db 316 EIMTRGQTPYVGIENAEYNYLLIGNRLKOPPECEMEDYDLYOCMSADPKORPSFTCLR 375
QY 761 MELENILAGLSVLSASODPLYNIERAE--EPTAGGSLELPGRD--OPTYGAGDGSOMG 815
Db 376 LQLEKLSLESLPDADAKESIIYINQULESCIEGIANGP-SLGLDWNIDPDSIIASCTPGA 434
QY 816 AVGTPTSDC-----RYIILPGSLAQPOGAHQPSPLNETNORLLILLOGLPHSSC 867

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DB	Accession	Score	DB	Length	Query
Db	435 AVSVYTAAEHNNLEEREYILNGCN--EEMEDVSSIPFAAYTPE-----KQGYLPEDD- 486	24.38	1137	DB 11	Query Match
QY	868 ADASLKADP 877	53.28	71	Mismatches 103; Indels 34; Gaps 10;	Best Local Similarity
Db	486 ---SPKMASP 492				Matches 236; Conservative
RESULT 13					
ID	060805	PRELIMINARY;	PRT;	994 AA.	
AC	060805				
DT	01-NOV-1996	(TREMBLrel. 01, Created)			
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)			
DT	01-NOV-1998	(TREMBLrel. 08, Last annotation update)			
DE	C-MER PROTOONCOGENE PRECURSOR (C-MER TYROSINE KINASE RECEPTOR).				
GN	MER.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;				
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
RN	[1]				
RP	SEQUENCE OF 1-315 FROM N.A.				
RC	STRAIN-B6; TISSUE-SPLEEN;				
RX	MEDLINE; 95303502.				
RA	GRAHAM D.K., BOWMAN G.W., DAWSON T.L., STANFORD W.L., EARP H.S.,				
RA	SNODGRASS H.R.;				
RT	"Cloning and developmental expression analysis of the murine c-mcr				
RL	tyrosine kinase." Oncogene 10:2349-2359(1995).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-B6; TISSUE-SPLEEN;				
RA	SNODGRASS H.R.;				
RL	Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; U21301; AA80222.1; .				
DR	MGI; MGI:96965; MER.				
DR	PFAM; PF00041; f03; 2.				
DR	PFAM; PF00047; f9; 2.				
DR	PFAM; PF00069; pkinase; 1.				
KW	Signal.				
FT	SIGNAL	1	20	POTENTIAL.	
FT	CHAIN	21	994	C-MER TYROSINE KINASE RECEPTOR.	
FT	SEQUENCE	994 AA;	110156 MW;	3C2P423D CRC32;	
QY	409 VVLG-----VTAVTAAALAILLRKRKRETRFGQAF---DSVAKREPAVHPAAASF 460	24.38	Score 1137; DB 11; Length 994;		
Db	499 IILGCFGLIIGLILCLSLA---LRRVQETKFGAGSEEDSQL-----VYVRAKRSF 550	53.28	71; Mismatches 103; Indels 34; Gaps 10;		
QY	461 NRERPERIEATLDSIGSIDELKELKEDLVLIPEOQFTIRMLGKGFGSVRAQKQEDGS 520				
Db	551 CR---RAIELTGLGLVSEELQNKLEIDVIDRNLVLGKVLGSEEFSGVMGKLNKQEDCT 607				
QY	521 FVKAVVMTKADIIASDIEFLREACMKFEFDPHYAKLVGSLRSKAKRLIPVYL 580				
Db	608 SQKAVATMTKIDNESQSEIEFLSEACMKFNPVYIRLGLVCIEELSSQ-IPKPVYL 666				
QY	581 PFMAHGLHAFILASRIGENPFNPLQTLIFWDIACGMEYLSRNPVHDLAARNOML 640				
Db	667 PFMAHGLHFLFLYSLRNLGPKYTHDITLFLKMDIAGMEYLSRNPVHDLAARNOML 726				
QY	641 AEDATCVADFGLSRKTIYSGDYRQGCASKLIPVYMLAESLADNLYTVQSDVMAFGVTM 700				
Db	727 RDMATVCAVADFGLSRKTIYSGDYRQGIAPKPVYKIIIESLADRVYTSKSDVMAFGVTM 786				
QY	701 EIMRGGTPTVAGIENATIVYLLIGGNLKKQPEMEDEYVYDLATMGCSNADPRQPSFTCLR 760				
Db	787 EITRGMTPYPGVONHEMYDYLHGHRLKKQPECDLDELXYIMWSCSNADPRDRTFVSLR 846				

OY 761 MELENIIGOLSVLSASODPLYINIERAE--EPTAGSLELPGRD---QPVSGAGDGSNG 815
DB 847 LQLEKLESIPDADKESIIYINQLESCGIANGP-SLTGIDMIDIPISITACPGA 905
OY 816 AVGTSPDC-----RYLTPG 831
DB 906 AVSVTAVEHNNLRERYILNGG 929

RESULT 14

ID 090777 PRELIMINARY; PRT; 974 AA.
AC 090777;
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 01-NOV-1998 (TRENBLREL. 08, Last annotation update)
DE C-EYK PROTO-ONCOGENE PROTEIN PRECURSOR.
GN C-EYK.
OS Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
[1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE; 94124527.
RA JIA R., HANAFUSA H.;
RT "The proto-oncogene of v-eyk (v-tyk) is a novel receptor-type protein
tyrosine kinase with extracellular Ig/GN-III domains."
RL J. Biol. Chem. 269:1839-1844(1994).
DR EMBL; L21719; AAC38010.1;
DR PFAM; PF00041; f03; 2.
DR PFAM; PF00047; f03; 2.
DR PFAM; PF00069; pkinase; 1.
KM Signal.
FT SIGNAL. 1 23 POTENTIAL.
FT CHAIN 24 974 C-EYK PROTO-ONCOGENE PROTEIN.
SQ SEQUENCE 974 AA; 106165 MW; E26ED23 CRC32;

Query Match 23.6%; Score 1102.5; DB 13; Length 974;
Best Local Similarity 48.2%; Pred. No. 2.5e-84;
Matches 235; Conservative 75; Mismatches 141; Indels 37; Gaps 9;

OY 409 VVLTALVTAALAL---ILLRKRKTRFGQAF---DSVWARPEVHRAARSEFR 462
DB 494 VALGFCGV-ANGILCSVIOKCMETKGNARSDS---ELVYNTAKSYCR 547
463 ERPERLEATLDSIGSDELKEDVLIPEOFTLGRMLGEGFSGVREAOIKOEDGSFV 522
548 ---RAVELTLGVSSELQKLDVDIRNALSLGKVLGSEFGVMEGRSLQEGTQ 604
OY 523 KVAVKRLKADITASSDIEEFLREDAKMEFDPHVAKLVSLSRANGRLPIPVILPF 582
DB 605 KVAVKTKMDNESHREIEFLEAACKMDPDPNVIKILGVCIELSSQ-QIPKPVILPF 663
OY 583 MKHGDLAFLASRIGENFENPLQTLIRFMDIACMEYSSRNFIHRDLAARCMAL 642
DB 664 MKYGDHSLSLSRLEMAFOVPLQMLKFWDLGMEYSSROFLHDLAARCMKMD 723
OY 643 DMTVCVADGSLSRKITYSGDIYRQGCASKLPRVWLALESIALDLYVQSDVAFVTAMEI 702
DB 724 DMTVCVADGSLSKITYSGDIYRQGCASKLPRVWLALESIALDLYVQSDVAFVTAMEI 783
OY 703 MKRGOTPAGINAEIYNLIGANLKPDPCEMEDVYDLMQCVADKORPSFTCLME 762
DB 784 MKRGOTPAGINAEIYNLIGANLKPDPCEMEDVYDLMQCVADKORPSFTCLME 843
OY 763 LENINGOLSVLSASODPLYINIERAE-----PTAGSLELPGRDPIYSGA 808
DB 844 LEKLESIPDADKESIIYINQLESCGIANGP-SLTGIDMIDIPISITACPGA 902
OY 809 GDGSGMAGVGTSPDCRYTLPGGLAEOPGAERHOPESPLNETQTLILQGLPHSSCA 868

DB 903 HKKALVAVDHIDGGRVYL-----ESGSPTEADAYVPLPHEGSAMTEASTLPVGSLL 956
OY 869 DASLKVAD 876
DB 957 AAOPLCAD 964

RESULT 15

ID 015516 PRELIMINARY; PRT; 600 AA.
AC 015516;
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 01-NOV-1998 (TRENBLREL. 08, Last annotation update)
DE TYROSINE KINASE.
OS Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
[1]
RP SEQUENCE FROM N.A.
RC TISSUE-TESTIS;
RX MEDLINE; 95327955.
RA BURKS D.J., CARBALLADA R., MOORE H.D., SALING P.M.;
RT "Interaction of a tyrosine kinase from human sperm with the zona
pellucida at fertilization."
RL Science 269:83-86(1995).
DR EMBL; L08961; AAC41766.1;
DR PFAM; PF00069; pkinase; 1.
KM Transmembrane.
SQ SEQUENCE 600 AA; 67874 MW; 54C9ACB0 CRC32;

Query Match 17.3%; Score 811; DB 4; Length 600;
Best Local Similarity 41.6%; Pred. No. 4.8e-60;
Matches 215; Conservative 73; Mismatches 125; Indels 104; Gaps 25;

OY 333 KYNTVALSC-----TCRG-SGNLQDCEQERSEFSON--PCLVEATAAKRFR- 380
DB 96 KINLTHIPCRGRPOPNVTCRDLKCNVSD---VORAMPGNVPC-----TRLR 144
OY 380 -QLF-SQOMASTFVVOQONSINPRKRVVYVGLVLTALVTAALAILLKRKRETF 437
DB 145 CPLENSGM-----ORRCAHMLMLMI-ILGLVLYSLA---TRKRVQETKF 190
OY 438 GOAF---DSVWARPEVHRAARSEFRPERLEATLDSIGSDELKEDVLIPEOQ 494
DB 191 GNAFTEDS-----ELVYNTAKSYCR---RAIELT-HSLGVSEELQKLEVDVIRNL 241
OY 495 FTGLMLGKGFSGVREAOIKOEDGSFVK--VAVKMLRADITASSDIEEFLREDAKMEF 552
DB 242 LILGKILGEGEKVYEGELMNIPEGKEVKKIPVAKTKLIDTMAN---KEIIDASVMKG 298
OY 553 DHPVAKIYVGLSLSRKGRPIPVILPEKRGDLAFLASRIGENFENPLQTLIRF 612
DB 298 GNPVAKIYVGLSLSRKGRPIPVILPEKRGDLAFLASRIGENFENPLQTLIRF 663
OY 613 MYDIACMEYSSRNFIHRDLAARCMALDPTCVADGSLSRKITYSGDIYRQGCASKL 672
DB 354 MYDIACMEYSSRNFIHRDLAARCMALDPTCVADGSLSRKITYSGDIYRQGCASKL 723
OY 673 VKTALSLADNLTYSQSDVAFVTAMEINT--RGOTPAGINAEIYNLIGANLKP 730
DB 414 VKTALSLADNLTYSQSDVAFVTAMEINT--RGOTPAGINAEIYNLIGANLKP 783
OY 731 PP-----EEME-----DYIDL-----MYQMSAD---PK 751
DB 473 PRMANCTEIRILKLPILGSRTRMPTITFSMATRISSPKAMNCKKCTLAGEBIPK 532
OY 752 ORPSFTCLMELENIIGOLSVLSASODPLYINIERAE 788
DB 533 TGPFVSYLRQLEKLESIPDADKESIIYINQLESCGIANGP-SLTGIDMIDIPISITACPGA 902

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 13, 1999, 02:20:29 ; Search time 33.26 Seconds

(without alignments)
679.590 Million cell updates/sec

Title: us-09-272-835-17

Sequence: 1 MVRPLNRPPLPPVYLMILL.....PWPSLFSCTLPILLISLM 369

Scoring table: BLOSUM62

Searched: 199794 seqs, 61255205 residues

Database:

SPTREMBL_11.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1993.5	98.6	400	4 060609	060609 homo sapien
2	1458	72.1	397	11 035118	035118 mus musculu
3	1455	72.0	397	11 055243	055243 mus musculu
4	1453	71.9	397	11 035225	035225 mus musculu
5	516	25.4	464	11 035977	035977 rattus norv
6	509	25.2	464	4 015316	015316 homo sapien
7	509	25.2	464	4 015328	015328 homo sapien
8	488	24.1	460	4 015507	015507 homo sapien
9	485.5	24.0	463	11 035252	035252 mus musculu
10	485.5	24.0	465	4 043912	043912 homo sapien
11	485.5	24.0	468	11 035246	035246 mus musculu
12	485	24.0	463	11 035748	035748 rattus norv
13	470	23.2	431	13 093512	093512 gallus gall
14	410	20.3	358	11 092243	092243 mus musculu
15	410	20.3	330	11 092242	092242 mus musculu
16	147.5	7.3	2704	5 097458	097458 drosophila
17	141	7.0	2653	5 025253	025253 lucilia cup
18	131	6.5	2195	5 020462	020462 caenorhabd
19	123	6.1	2026	4 000468	000468 homo sapien
20	122.5	6.1	1964	11 035442	035442 mus musculu
21	121	6.0	3857	11 088840	088840 mus musculu
22	118.5	5.9	1989	4 099940	099940 homo sapien
23	118.5	5.9	2003	4 000306	000306 homo sapien
24	118.5	5.9	955	4 099466	099466 homo sapien
25	114.5	5.7	850	4 095804	095804 homo sapien
26	113.5	5.6	1034	11 035888	035888 rattus norv
27	111.5	5.5	1095	11 060788	060788 mus musculu
28	111	5.5	2019	11 064706	064706 mus musculu
29	110.5	5.5	5376	11 088799	088799 mus musculu

30	109	5.4	1661	5 077244	077244 chlorohydra
31	109	5.4	1203	11 006008	006008 mus musculu
32	109	5.4	4545	11 061291	061291 mus musculu
33	109	5.4	2470	11 035516	035516 mus musculu
34	108.5	5.4	2150	5 044131	044131 caenorhabd
35	107.5	5.3	1254	13 097802	097802 brachydanto
36	107	5.3	1792	13 057484	057484 gallus gall
37	106	5.2	838	5 018482	018482 opilliaspon
38	105.5	5.2	473	5 025464	025464 mytilus gal
39	105	5.2	448	4 075965	075965 homo sapien
40	104.5	5.2	3507	5 023587	023587 caenorhabd
41	104	5.1	1722	5 019350	019350 caenorhabd
42	103.5	5.1	2352	5 061240	061240 halocynthia
43	103.5	5.1	1296	5 022452	022452 caenorhabd
44	103.5	5.1	2531	5 016004	016004 lytechinus
45	103	5.1	1704	5 094446	094446 chironomus

ALIGNMENTS

RESULT 1
ID 060609 PRELIMINARY; PRT; 400 AA.
AC 060609;
DT 01-AUG-1998 (TRENBERL. 07, Created)
DT 01-AUG-1998 (TRENBERL. 07, Last sequence update)
DT 01-AUG-1998 (TRENBERL. 07, Last annotation update)
DE GDNF FAMILY RECEPTOR ALPHA 3.
GN GFR3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA BALOH R.H., GORODINSKY A., GOLDEN J.P., TANSEY M.G., KECK C.L.,
RA POBESCU N.C., JOHNSON E.M. JR., MILBRANDT J.,
RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(1998).
DR EMBL: AF051767; AAC2435.1;
SQ SEQUENCE 400 AA; 44538 MW; 6DFB5361 CRC32;

Query Match 98.6%; Score 1993.5; DB 4; Length 400;
Best Local Similarity 92.0%; Pred. No. 9.3e-195;
Matches 368; Conservative 1; Mismatches 0; Indels 31; Gaps 1;

QY	1	MVRPLNRPPLPPVYLMILLPPSPPLAAGDPLPTESRLMNSCLARRKQADPTCSAA	60
DB	1	MVRPLNRPPLPPVYLMILLPPSPPLAAGDPLPTESRLMNSCLARRKQADPTCSAA	60
QY	61	YHNDSTSSISTPSPSESPVADCLAAQOLRNSLIGCMCHRRKKNQVACLDITWTY	120
DB	61	YHNDSTSSISTPSPSESPVADCLAAQOLRNSLIGCMCHRRKKNQVACLDITWTY	120
QY	121	HRARSL-----DSGLCKEFLMTINDKCRRLK	149
DB	121	HRARSLNLTVDSPEDYTSFPMKNTSKLMLKPDSDLCIKFMTLTDKCRRLK	180
QY	150	AYEAGSGPHQCRHVCLKOLLTFEERKAEPHAGLLICAPNDRCGERRRTIPNCA	209
DB	181	AYEAGSGPHQCRHVCLKOLLTFEERKAEPHAGLLICAPNDRCGERRRTIPNCA	240
QY	210	LPVPAPNCLERLRCFSDPLCRRLVDFTGHPMDILTCATGSRCLRAVIGLGTAM	269
DB	241	LPVPAPNCLERLRCFSDPLCRRLVDFTGHPMDILTCATGSRCLRAVIGLGTAM	300
QY	270	TPPFSVNTSVALLSCGSGNLOEGECMLTGEFSHNCIETAIKKRFSQFSQW	329
DB	301	TPPFSVNTSVALLSCGSGNLOEGECMLTGEFSHNCIETAIKKRFSQFSQW	360
QY	330	PHPTFAVMAHONENPAVRPOPWPVPSLFSCTLPILLISLM	369
DB	361	PHPTFAVMAHONENPAVRPOPWPVPSLFSCTLPILLISLM	400

DE 01-JUN-1998 (Triemlrel. 06, last annotation family)
DR GLIUM CELL LINE-DERIVED NEUROGENIC FACTOR RECEPTOR ALPHA-3
GN GFA3.
OS Mus musculus (Mouse).
OC Euteleostei; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RA WIDENFALK J., TOMAC A., LINDVIST E., HOFER B., OLSON L.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA NAVEILHAN P., BAUDET C., MIKAELS O., SHEN L., WESTPHAL H.,
RA ERNFORS P.;
RA Proc. Natl. Acad. Sci. U.S.A. 0:0-0(1997).
DR EMBL: AF041842; AAC24558.1; -
DR EMBL: AF036163; AAC24448.1; -
SO SEQUENCE 397 AA; 44302 MW; F77607CF CRC32;

Query Match Similarity	72.0%	Score 1455	DB 11	Length 397
Best Local Similarity	69.4%	Pred. No. 4.8e-140		
Matches	275	Conservative	30	Mismatches 59; Indels 32; Gaps 2

Query	5	LNRPRLPPVYVLTMLLLPSPPLPLAAGDPLPTESRLMNSCLQARRKQCAPDPTCSAAHYHL	64
Db	3	LSLEPRRP-LIMILLVYLSIMPLPLAGNSLTATENFVNSCTQARRKCEANPCKAAVQHL	61
QY	65	DSCTSSISTPLPSESPVPADCLFAAQQLRNSSLIGCMCHRMKNQVACLDIYTWVHARR	124
Db	62	GSCSTSLRPPLPESASADCLFAEQLRNSSLIDCRCRHRMKHQATCLDIYTWVHARR	121
QY	125	SL-----DSIDLKFMALCTINDKCRKRAYE	153
Db	122	SLGDELVYSPEDYVTKPMKRNLSKTNMLKPDSDLCIKFEMALCTLHDKCRKRAYE	181
QY	154	ACSGPCHQAHVCLROLTLTFEKAAPHAQGLLACPAENDRCGERRRTIAPNCALPV	213
Db	182	ACSGIRCCRHLCQLQALRSFEKAAESHAGLLCCPPEADGCGRRRTIAPNCALPV	241
QY	214	APNCLERLRFSPDLCKSLVDYFOTGHCPMDILGTCATEGSRCLRAYIGLIGTAMPNF	273
Db	242	TENCNDLHSFRADPLCKSRIMDFOTGHCPMDIILGTCATEGSRCLRAYIGLIGTAMPNF	301
QY	274	VSNTVAALSCCTCGSGNLTDECEMLEGFSHNPCLAEATAAKRRFSOLFOWPHEPT	333
Db	302	ISKNTVYALSCCTCGSGNLTDECEQLSRSSQNCVLEATIAAKRRFROLFOWPMAST	361
QY	334	FAYNAHONENPVRPOPVPVPSLFCSTPLILLLSLM	369
Db	362	FSVVOGQNSNAPLRLQPLRLPILSILPLILLQITLM	397

RESULT	4	
ID	035325	PRELIMINARY; PRT; 397 AA.
AC	035325	
DT	01-JAN-1998	(TIEMBLrel. 05, Created)
DT	01-JAN-1998	(TIEMBLrel. 05, Last sequence update)
DT	01-AUG-1998	(TIEMBLrel. 07, Last annotation update)
DE	GLIAL CELL LINE-DERIVED NEUROTROPIC FACTOR FAMILY RECEPTOR ALPHA-3.	
GN	GERA-1.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
RN	[1]	
RA	SEQUENCE FROM N.A.	
RP	TRUPP M., RAYNOSCHER C., IBANEZ C.F.;	
RR	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.	
RL	EMBL: AF020305; MAF70931.1;	
SQ	SEQUENCE 397 AA; 44333 MW; F0CC0C841 CRC32;	

QY 125 -SLDSDCLFAMLCITNDKCDRLKAYGACS-----GPHCORHVCRLQLLTFEKKAE 178
 DB 154 VSANSMCHLDAAACNLDNCKLRSSYSICNREISPTERCNRCKHRLRQFDRVPS 213
 QY 179 PHAGGLICPCAPNDRCGGERRRRTIAPNCAL-PPVAPNLELRRLCPSPLCRSLVDF 237
 DB 214 EYTRMLFCCSC--QODACARRRGTILPSCSYDEKRPNCDLRGVCRDHLCRSLADF 271
 QY 238 QTRCHP--MDILGTCATEOSRCLRAYLGLIGTAMTPEFVNVTVALS--CTCRSGNLT 293
 DB 272 HANCRASTYQVTSQPADNYAGACISGYAGMGFMTPTVYDVSPTGLVYVWCSCRSNGM 331
 QY 294 QEECEMLEGFFSHNPCLTEAIAA 316
 DB 332 EEECEKFLRDFTENPCIRNAIOA 354
 RESULT 7
 015328 PRELIMINARY: PRT; 464 AA.
 015328; 015328;
 01-JAN-1998 (TREMREL. 05, Created)
 01-JAN-1998 (TREMREL. 05, Last sequence update)
 01-NOV-1998 (TREMREL. 08, Last annotation update)
 DE RET LIGAND 2.
 GN RETL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LIVER;
 RX MEDLINE: 97322356.
 RA SANICOLA M., HESSION C.A., WORLEY D.S., CARMILLO P., EHRENFELS C.,
 RA WALUS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
 RA PEPINSKY R.B., CATE R.L.,
 RT "Glial cell line-derived neurotrophic factor-dependent RET activation
 can be mediated by two different cell-surface accessory proteins."
 RL Proc. Natl. Acad. Sci. U.S.A. 94:6238-6243(1997).
 DR EMBL: U97145; AAC51647.1;
 SO SEQUENCE 464 AA; 51543 MW; 288A8BD8 CRC32;

Query Match 25.2%; Score 509; DB 4; Length 464;
 Best Local Similarity 34.4%; Pred. No. 7.4e-44;
 Matches 111; Conservative 41; Mismatches 113; Indels 58; Gaps 8;
 44 CIOARRKQADPTCSAAHYHLDSCFS--SISTPLSEEPSVPADCLEAAOQLNSSLIGC 101
 40 CVANFELCAESNCSSRYRTLROCLAGRDRTMLANKE-----COALEVLQESPLYDC 93
 QY 102 MCHRRKNOVACLDIYTVYHAR----- 125
 DB 94 RCKRGKRLQCLQIYNSHGLTEGEETYSPEVPTSRLSDIFRLASITSGADPV 153
 QY 125 -SLDSDCLFAMLCITNDKCDRLKAYGACS-----GPHCORHVCRLQLLTFEKKAE 178
 DB 154 VSANSMCHLDAAACNLDNCKLRSSYSICNREISPTERCNRCKHRLRQFDRVPS 213
 QY 179 PHAGGLICPCAPNDRCGGERRRRTIAPNCAL-PPVAPNLELRRLCPSPLCRSLVDF 237
 DB 214 EYTRMLFCCSC--QODACARRRGTILPSCSYDEKRPNCDLRGVCRDHLCRSLADF 271
 QY 238 QTRCHP--MDILGTCATEOSRCLRAYLGLIGTAMTPEFVNVTVALS--CTCRSGNLT 293
 DB 272 HANCRASTYQVTSQPADNYAGACISGYAGMGFMTPTVYDVSPTGLVYVWCSCRSNGM 331
 QY 294 QEECEMLEGFFSHNPCLTEAIAA 316
 DB 332 EEECEKFLRDFTENPCIRNAIOA 354

015507
 ID 015507 PRELIMINARY: PRT; 460 AA.
 AC 015507;
 DT 01-JAN-1998 (TREMREL. 05, Created)
 DT 01-JAN-1998 (TREMREL. 05, Last sequence update)
 DT 01-NOV-1998 (TREMREL. 08, Last annotation update)
 DE RET LIGAND 1.
 GN RETL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-KIDNEY;
 RX MEDLINE: 97322356.
 RA SANICOLA M., HESSION C.A., WORLEY D.S., CARMILLO P., EHRENFELS C.,
 RA WALUS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
 RA PEPINSKY R.B., CATE R.L.,
 RT "Glial cell line-derived neurotrophic factor-dependent RET activation
 can be mediated by two different cell-surface accessory proteins."
 RL Proc. Natl. Acad. Sci. U.S.A. 94:6238-6243(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-KIDNEY;
 RX MEDLINE: 97322356.
 RA SANICOLA M., HESSION C.A., WORLEY D.S., CARMILLO P., EHRENFELS C.,
 RA WALUS L., ROBINSON S., JAMORSKI G., WEI H., TIZARD R., WHITTY A.,
 RA PEPINSKY R.B., CATE R.L.,
 RL Submitted (APR-1997) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-SUBSTANTIA NIGRA;
 RA HISHIKI T., KONDOH K., ICHIMITA S., NIMURA Y., SEKI N., OZAKI T.,
 RA SAKIYAMA S., TAKAHASHI H., OHNUMA N., TANABE M., FUJIMURA S.,
 RA NAKAGAWARA A.,
 RL Submitted (OCT-1997) to the EMBL/Genbank/DBJ databases.
 DR EMBL: U97144; AAC51646.1;
 DR EMBL: U95847; AAB71811.1;
 SO SEQUENCE 460 AA; 50838 MW; 022FEBCA CRC32;

Query Match 24.1%; Score 488; DB 4; Length 460;
 Best Local Similarity 34.7%; Pred. No. 1e-41;
 Matches 121; Conservative 42; Mismatches 122; Indels 64; Gaps 11;
 QY 17 LLLPLPPLPLAA-----GDLPTESRLMNSCLQARRKQADPTCSAAHYHLDSCFS-- 70
 DB 6 LYFALPLDLILLSAEVSGDRL-----DCVYASDQCLEQSCSTYRTLROCVAKKE 57
 QY 70 --SISTPLSEEPSVPADCLEAAOQLNSSLIGCMCHRRKNOVACLDIYTVYHAR--- 124
 DB 58 TNSLSAGLEAKD-----ECSRAMEALNOKSLYNCRCRKGKKEKNCRLITVSMYQSLQG 112
 QY 124 -----RSLSDCL-----CLKFAMLCTLNDKCDRLKAYGEA 154
 DB 113 NDLEDSPYEYVNSRLSDIFRVVPFISVEHLPKNNCNDAAKACNLDIDICKIYSATITP 172
 QY 155 C---SGPHCORHVCRLQLLTFEKKAEPPHAGGLICPCAPNDRCGGERRRRTIAPNCAL 210
 DB 173 CITSVDYCNRRCKHRLRQFDPKVPKHSYGMFCSG--RDIACTERRRGTIVPVCS 230
 QY 211 PP-VAPNLELRRLCPSPLCRSLVDFQTRCHMD--ILGTCATEQ--SRCLRAYLGLIGT 267
 DB 231 EEREKPNCLNQDSCCKTYIKRSLADFTNCPQEPSNSVSSCLLENVADCLAYSLIGT 290
 QY 268 AMTPEFVNVTVALSCTCRSGNLTQEECEMLEGFFSHNPCLTEAIAA 316
 DB 291 VMTPTVIDSSLSVAPMCDSCNSGNDLEECLEKFLNFRDNTCLNNAIOA 339
 RESULT 9
 035252 PRELIMINARY: PRT; 463 AA.
 ID 035252
 AC 035252;

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DR 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DE GDNF RECEPTOR BETA.
GN GDNFR-BETA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
NC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RP SEQUENCE FROM N.A.
RC STRAIN-C57.
RA DEY B.K., KONG Y.W., TOO H.P.;
RL NeuroReport 9:0-0(0001).
[2]
RC STRAIN-C57;
RA DEY B.K., KONG Y.W., TOO H.P.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
EMBL: AF015172; AAB86600.1;
SEQUENCE 463 AA; 51134 MW; 910EF17F CRC32;

Query Match          24.1%; Score 487; DB 11; Length 463;
Best Local Similarity 34.5%; Pred. No. 1.3e-41;
Matches 130; Conservative 44; Mismatches 122; Indels 62; Gaps 11;

QY 14 VLMILLPPSPPLAAGDPLPTESRLMNSCLARRKQADPTCSAAYHHLDSTS--- 70
DB 9 VLPLDLMLMA--EVSGDRL-----DCVKASDQCLKQSCSTKRYRLRQCVAKE 58
QY 70 --SISPLPSEEPSVPADCLEAAQOLRNSSLIGCMCHRMKNQVACLDIYTVHRA--- 124
DB 59 NFSITSGLEAKD-----ECSSAMEALKOKSLYNCRCKRGMKEKNCIRITYSMTQSLQGN 113
QY 124 -----RSLDSDL-----CLKFAMLTGLNDKCDRLKRAYGEAC 155
DB 114 DLLEDSPYEPVNSRLSDIFRAVPFISVEHISKGNCLDAKACNLDDTCCKYRSAYITPC 173
QY 156 ----SGPHCOHVCRLQRLTFEKEAEPHAGLILPCAPDRGCGERRNTAPNCALP 211
DB 174 TTSMSNVNCRKCHKALROFDFKVPKHSYGLMFCSC--RDVACERRRQTIYVPCSYE 231
QY 212 P-VAPNCLRLRCLFSDPLCRSLVDFTQCHPMD-ILGTCAEQ--SRCLRAYLGLGTA 268
DB 232 ERRRPCLNLDQSCCKNYICRSLADFTNCOESRSVSCLEKNYADCLLAYSGLGTV 291
269 MTPNYSNNTSVALSCTCRGSGNLQECCEMLGFFSHNPCLTEAIA 316
292 MPNYSIDSSLSVAPMCDSCNSGNDLECLKFNFMDNCTCKNAIOA 339

RESULT 10
ID 043912 PRELIMINARY; PRT; 465 AA.
AC 043912;
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
DE 01-AUG-1998 (TREMblrel. 07, Last annotation update)
DE GFI-LINKED ANCHOR PROTEIN.
GN GFI-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
NC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RP SEQUENCE FROM N.A.
RA ANGRIST M., JING S., BOLT S., BENTLEY K., NALLASAMY S., HALUSHKA M.,
RC FOX G.M., CHARRAVARTI A.;
RL Genomics 0:0-0(1998).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE-MEDULLARY THYROID CARCINOMA TUMOR;
RA SHEPHERD S.E., KHORANA S., SCHULTZ P.N., HUANG E., THORBE N.,
RL HU Z.J., FOX G.M., JING S., COTE G.J., GAGEL R.F.;

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RL Hum. Genet. 0:0-0(1998).
DR EMBL: AF038420; AAC39693.1;
DR EMBL: AF038411; AAC39693.1; JOINED.
DR EMBL: AF038412; AAC39693.1; JOINED.
DR EMBL: AF038413; AAC39693.1; JOINED.
DR EMBL: AF038414; AAC39693.1; JOINED.
DR EMBL: AF038415; AAC39693.1; JOINED.
DR EMBL: AF038416; AAC39693.1; JOINED.
DR EMBL: AF038417; AAC39693.1; JOINED.
DR EMBL: AF038418; AAC39693.1; JOINED.
DR EMBL: AF038419; AAC39693.1; JOINED.
DR EMBL: AF042080; AAB97271.1;
DR EMBL: AF038421; AAC39692.1;
DR EMBL: AF058999; AAC14431.1;
DR EMBL: AF058990; AAC14431.1; JOINED.
DR EMBL: AF058991; AAC14431.1; JOINED.
DR EMBL: AF058992; AAC14431.1; JOINED.
DR EMBL: AF058993; AAC14431.1; JOINED.
DR EMBL: AF058994; AAC14431.1; JOINED.
DR EMBL: AF058995; AAC14431.1; JOINED.
DR EMBL: AF058996; AAC14431.1; JOINED.
DR EMBL: AF058997; AAC14431.1; JOINED.
DR EMBL: AF058998; AAC14431.1; JOINED.
SQ SEQUENCE 465 AA; 51455 MW; 1C4EAE03 CRC32;

Query Match          24.0%; Score 485.5; DB 4; Length 465;
Best Local Similarity 34.2%; Pred. No. 1.8e-41;
Matches 121; Conservative 42; Mismatches 122; Indels 69; Gaps 11;

QY 17 LLLLLPPSPPLA---GDPLPTESRLMNSCLARRKQADPTCSAAYHHLDSTS--- 70
DB 6 LYFALPLDLILLSAEVSGDRL-----DCVKASDQCLKQSCSTKRYRLRQCVAKE 57
QY 70 ---SISPLPSEEPSVPADCLEAAQOLRNSSLIGCMCHRMKNQVACLDIYTVHRA--- 124
DB 58 TNSLSASGLEAKD-----ECSSAMEALKOKSLYNCRCKRGMKEKNCIRITYSMTQSLQGN 112
QY 124 -----RSLDSDL-----CLKFAMLTGLNDKCDRLK 149
DB 113 NDLEDSPYEPVNSRLSDIFRAVPFISVFOVEHLPKSNCLDAKACNLDDTCCKYRS 172
QY 150 AYEDAC----SGPHCOHVCRLQRLTFEKEAEPHAGLILPCAPDRGCGERRNTA 205
DB 173 AYTPCTSVSNVNCRRKCHKALROFDFKVPKHSYGLMFCSC--RDVACERRRQTIY 230
QY 206 PNCALP-VAPNCLRLRCLFSDPLCRSLVDFTQCHPMD-ILGTCAEQ--SRCLRAYL 262
DB 231 PVSYYEERKPNCLNLDQSCCKNYICRSLADFTNCOESRSVSCLEKNYADCLLAYS 290
QY 263 GLIGTAMTPNYSNNTSVALSCTCRGSGNLQECCEMLGFFSHNPCLTEAIA 316
DB 291 GLIGTAMTPNYSIDSSLSVAPMCDSCNSGNDLECLKFNFMDNCTCKNAIOA 344

RESULT 11
ID 035246 PRELIMINARY; PRT; 468 AA.
AC 035246;
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DE 01-JAN-1998 (TREMblrel. 05, Last annotation update)
DE GDNF RECEPTOR ALPHA.
GN GDNFR-ALPHA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
NC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RP SEQUENCE FROM N.A.
RC STRAIN-C57; TISSUE-LIVER;
RA DEY B.K., KONG Y.W., TOO H.P.;
RL NeuroReport 9:0-0(0001).
[2]

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RP SEQUENCE FROM N.A.
RC STRAIN-C57; TISSUE=LIVER;
RA DEY B.R.; MONG Y.W.; TOO H.P.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF014117; AAB6599.1;
SQ SEQUENCE 468 AA; 51751 MW; APCDE6A1 CRC32;

Query Match 24.0%; Score 485.5; DB 11; Length 468;
Best Local Similarity 34.3%; Pred. No. 1.8e-41;
Matches 121; Conservative 42; Mismatches 123; Indels 67; Gaps 11;

QY 14 VLMLLLPSPPLAAGDPLPTESRLMNSCLQARRKQADPTCSAAVHHLDSCTS--- 70
DB 9 VLPLDLMLSA--EYSGGDL-----DCVKASDCLKFGSCSTKRLRQCVAGRET 58
QY 70 --SISTPLSEPSVPACDLAQAOLRNSSLIGCMCHRRMNOVACDIYTVH----- 122
DB 59 NFSLSGLAEND-----ECRSAMELKKOKSLYNCRCKRGMKKNCLNTYSMYSLOGN 113
QY 122 -----RARSLSDL-----CLKFAMLCTLNDKCDRLRKA 150
DB 114 DLDESPYEPVNSRLSDIFRAVPFISDVFQVEHISKGNLDAKACNLDLDTCKKTRSA 173
QY 151 YGEAC---SGPHQRHVCLRLQLTFEKAEPHAGLLCPCAPNDRCGERRRNTIAP 206
DB 174 YITPCTMSNEVCNRRKCHALROFEDKVPKAKSYGMLFCSC--RDVACTERRQITVP 231
QY 207 NCALPP--VAPNCLERLRCFSDPLCRSLVDFOHCHMD--ILGTCAEQ--SRCLRAYLG 263
DB 232 VCSIEEREPNCLNDQSCRTNYCRSLADFENCPESHRSVSNCKENYADCLLAYSG 291
QY 264 LIGTAMPNPNVSNVTSVALSCTRGSGNLQEECEMLEGFSHNPCLTEAIA 316
DB 292 LIGVTMPNPNYIDSSLSVAAPWCDCNSGNDLDELKPLNFKDNTCLKNAIOA 344

RESULT 12
ID 035748 PRELIMINARY; PRT; 463 AA.
AC 035748;
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT 01-JAN-1998 (TREMblrel. 05, Last annotation update)
DE GDNF-ALPHA/TRN1-DELTA PROTEIN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Rattus.
[1]
SEQUENCE FROM N.A.
RC STRAIN=HANNOVER;
RA ZHONG J.; ANNIES M.; HEUMANN R.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ002072; CA005171.1;
SQ SEQUENCE 463 AA; 51032 MW; 93277F91 CRC32;

Query Match 24.0%; Score 485; DB 11; Length 463;
Best Local Similarity 34.4%; Pred. No. 2e-41;
Matches 120; Conservative 42; Mismatches 123; Indels 64; Gaps 11;

QY 17 LLLPLPSPPLA---GDPLPTESRLMNSCLQARRKQADPTCSAAVHHLDSCTS--- 70
DB 6 LYLALPLDLMLSAFVSGGDL-----DCVKASDQCLKEGSCSKYRTLRLQCVAGRE 57
QY 70 ---SISTPLSEPSVPACDLAQAOLRNSSLIGCMCHRRMNOVACDIYTVHRA--- 124
DB 58 TNSLSVIGLEAKD-----ECRSAMELKKOKSLYNCRCKRGMKKNCLNTYSMYSLOG 112
QY 124 -----RARSLSDL-----CLKFAMLCTLNDKCDRLRKA 154
DB 113 NDLLSDPYEPVNSRLSDIFRAVPFISVETISKGNLDAKACNLDLDTCKKTRSAITTP 172

QY 155 C---SGPHQRHVCLRLQLTFEKAEPHAGLLCPCAPNDRCGERRRNTIAPCAL 210
DB 173 CTSMSNEVCNRRKCHALROFEDKVPKAKSYGMLFCSC--RIACTERRQITVPYCSY 230
QY 211 PP-VAPNCLERLRCFSDPLCRSLVDFOHCHMD--ILGTCAEQ--SRCLRAYLG 267
DB 231 EERERPNCLELQSCRTNYCRSLADFENCPESHRSVSNCKENYADCLLAYSG 290
QY 268 AMPNPNVSNVTSVALSCTRGSGNLQEECEMLEGFSHNPCLTEAIA 316
DB 291 VMPNPNYIDSSLSVAAPWCDCNSGNDLDELKPLNFKDNTCLKNAIOA 339

RESULT 13
ID 093512 PRELIMINARY; PRT; 431 AA.
AC 093512;
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
DE GFR RECEPTOR ALPHA 4 PRECURSOR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96313402.
RA THOMPSON J.; DOXATIS E.; PINON L.G.; STRACHAN P.; BUI-BELLO A.;
RA WYATT S.; BUCHANAN V.L.; DAVIES A.M.;
RT "GFRalpha-4, a new GDNF family receptor".
RL Mol. Cell. Neurosci. 11:117-126(1998).
DR EMBL: AF045162; AAC36464.1;
KW Signal.
FT SIGNAL. 1 17. POTENTIAL.
FT CHAIN 18 431. GFR RECEPTOR ALPHA 4.
SQ SEQUENCE 431 AA; 47964 MW; 7AE1F0B0 CRC32;

Query Match 23.2%; Score 470; DB 13; Length 431;
Best Local Similarity 33.3%; Pred. No. 6.3e-40;
Matches 105; Conservative 32; Mismatches 132; Indels 46; Gaps 8;

QY 44 CLQARRKQADPTCSAAVHHLDSCTSISIPLSEPSVPACDLAQAOLRNSSLIGCMC 103
DB 26 CLQAGSSCNDRPLCSSKFKRLKOCIA--GNGANKLPDAKNQCRSTVTALLSQLGCKC 83
QY 104 HRPMQVACLDIYTVHRA-----RSLD-----SD 129
DB 84 KRGMKEKHCISYVSIHHTLMGMNVLESPEPEPIRGFDYRLASITAGSENEYOVN 143
QY 130 LCLAFMLCTLNDKCDRLRKA 184
DB 144 KCLDAKACNVEMCCQLRTEYVSFCIRLARADTCNRKCHALRKFDRVPPEYTHEL 203
QY 185 LCPAPNDRCGERRRNTIAPCAL--PPVAPNCLERLRCFSDPLCRSLVDFOHCHP 243
DB 204 LCPQC--EDTACAEKRQITVPACSTESKEKFWCLAPLDSCHRENYCRVAIFQNCOP 261
QY 244 -MDILGTCAEQ--SRCLRAYLGIGTAMPNPNVSNVTSVALSCTRGSGNLQEECEMLE 301
DB 262 SLQASGCRDSDVAACLLAYTGIIIGSPIIPNIDNTSSIAFQCTONASGNGQECESFL 321
QY 302 GFSHNPCLTEAIA 316
DB 322 HLFIDNVCLQNAIOA 336

RESULT 14
ID 0922A3 PRELIMINARY; PRT; 358 AA.
AC 0922A3;
DT 01-MAY-1999 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 12, 1999, 20:17:04 : Search time 27.76 seconds

(without alignments)
1508.874 Million cell updates/sec

Title: US-09-272-835-20

Perfect score: 4675
Sequence: 1 MGSTARLGAIVLFTVIVGL.....DASLRKADPNRFRCKDLPVL 888

Scoring table: BLOSUM62

arched: 142080 seqs, 47169319 residues

-cbase :

PIR-62: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2403	51.4	890	1	A53743	protein-tyrosine k
2	2399	51.3	882	2	I38912	receptor tyrosine
3	2337.5	50.0	723	2	I38412	receptor tyrosine
4	2257	48.3	880	1	JC4166	protein-tyrosine k
5	2246	48.0	880	2	B53743	protein-tyrosine k
6	2246	48.0	876	2	I49152	protein-tyrosine k
7	2080	44.5	856	2	I58411	protein-tyrosine k
8	1880	40.2	397	2	JE0082	GPI-linked recepto
9	1204.5	25.6	834	1	A41577	protein-tyrosine k
10	1178.5	25.2	898	2	S23065	ufo protein - mous
11	1155.5	24.7	999	2	I38547	novel cellular pro
12	1137	24.3	994	2	I49276	c-mer tyrosine kin
13	1130.5	24.2	942	2	S23251	protein-tyrosine k
14	1102.5	23.6	974	1	A49714	protein-tyrosine k
15	1061.5	22.7	442	1	B43362	protein-tyrosine k
16	811	17.3	600	2	A56379	protein-tyrosine k
17	696	14.9	1369	1	JC4860	env-sea polyprotel
18	662.5	14.2	596	1	TVFVSA	protein-tyrosine k
19	658.5	14.1	1404	1	A48196	protein-tyrosine k
20	645.5	13.8	1378	1	I48751	protein-tyrosine k
21	615.5	13.2	1379	1	S01254	hepatocyte growth
22	613	13.1	1375	1	JC5148	hepatocyte growth
23	612.5	13.1	1367	1	IGHUR1	hepatocyte growth
24	610	13.0	2554	1	TVF77L	insulin-like growt
25	609.5	13.0	640	2	S23068	kinase-related pro
26	606	13.0	1380	1	TVHUME	insulin-like growt
27	600	12.8	1400	1	I38185	hepatocyte growth
28	596	12.7	1371	2	A33837	insulin-like growt
29	590.5	12.6	1115	1	S29926	protein-tyrosine k
30	587	12.6	2594	2	A53774	protein-tyrosine k
31	586.5	12.5	1382	1	INHR	kinase-related pro
32	585	12.5	1550	1	TVFVSA	insulin receptor p
33	583.5	12.5	899	2	I38153	gene retill protein
34	579.5	12.4	1372	2	A34157	insulin receptor p
35	576.5	12.3	1064	1	S57450	insulin receptor p
36	574.5	12.3	1383	2	A36080	insulin receptor p
37	573.5	12.3	1114	1	S05882	protein-tyrosine k
38	570.5	12.2	1300	2	A36502	insulin receptor-t
39	570.5	12.2	981	1	FOHGM	gag-abl polyprotel

40	569	12.2	1123	2	A39962	kinase-related tra
41	568.5	12.2	402	1	TVFYUR	protein-tyrosine k
42	568	12.1	801	4	TVHUME	transforming prote
43	566.5	12.1	402	2	B34735	protein-tyrosine k
44	566	12.1	477	2	JN0291	protein-tyrosine k
45	565.5	12.1	873	2	S60740	protein-tyrosine k

ALIGNMENTS

RESULT 1
A53743
protein-tyrosine kinase (EC 2.7.1.112) tyros precursor - human
N:Alternate names: protein-tyrosine kinase sky; receptor-type tyrosine kinase rse
C:Species: Homo sapiens (man)
C>Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text, change 10-Sep-1999
C:Accession: A53743; J00777; J02145; S32765; S32219
R:Mark, M.R.; Scadden, D.T.; Wang, Z.; Gu, Q.; Goddard, A.; Godowski, P.J.
J. Biol. Chem. 269, 10720-10728, 1994
A>Title: rse, a novel receptor-type tyrosine kinase with homology to Ax1/Ufo, is expr
A:Reference number: A53743; M01D:94193774
A:Accession: A53743
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-890 <MAN>
A:Cross-references: GB:U05682; NID:9463469; PIDN:AAA19236.1; PID:9463470
R:Ohashi, K.; Mizuno, K.; Kuma, R.; Miyata, T.; Nakamura, T.
Oncogene 9, 699-705, 1994
A>Title: Cloning of the cDNA for a novel receptor tyrosine kinase, sky, predominantly
A:Reference number: J00777; M01D:94150991
A:Accession: J00777
A:Molecule type: mRNA
A:Residues: 1-890 <MAN>
A:Cross-references: DDBJ:D17517; NID:9624880; PIDN:BAA04467.1; PID:d1004992; PID:9624
A:Experimental source: hepatoma Hep3 cell
R:Polvi, A.; Armstrong, E.; Lai, C.; Lemke, G.; Huebner, K.; Sirtz, R.A.; Guida, L.C
Gene 114, 289-293, 1993
A>Title: The human TYRO3 gene and pseudogene are located in chromosome 15q14-q25.
A:Reference number: J02145; M01D:94085793
A:Accession: J02145
A:Molecule type: mRNA
A:Residues: 519-790 <POL>
A:Cross-references: EMBL:X72886; NID:9286020; PIDN:CAA51396.1; PID:g312336
R:Polvi, A.; Armstrong, E.; Lai, C.; Lemke, G.; Huebner, K.; Sirtz, R.A.; Guida, L.C
Submitted to the EMBL Data Library, March 1993
A>Description: Human TYRO3 gene and pseudogene in chromosome 15pter-q25.
A:Reference number: S32765
A:Accession: S32765
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 519-790 <POL>
A:Cross-references: EMBL:X72886; NID:9286020; PIDN:CAA51396.1; PID:g312336
C:Genetics:
A:Gene: GDB:TYRO3
A:Cross-references: GDB:134764; OMIM:600341
A:Map position: 15q15.1-15q21.1
C:Superfamily: protein-tyrosine kinase axl; fibronectin type III repeat homology; imm
C:Keywords: ATP; brain; glycoprotein; growth factor receptor; phosphotransferase; tra
F:1-41/Domain: (or 7-41) signal sequence #status predicted <SIG>
F:42-990/Product: protein-tyrosine kinase tyros #status predicted <MAN>
F:60-119/Domain: immunoglobulin homology <IMM2>
F:156-205/Domain: immunoglobulin homology <IMM2>
F:224-309/Domain: fibronectin type III repeat homology <FN3A>
F:322-405/Domain: fibronectin type III repeat homology <FN3B>
F:429-451/Domain: transmembrane #status predicted <MAN>
F:516-793/Domain: protein kinase homology <KIN>
F:524-532/Region: protein kinase ATP-binding motif
F:63,191,230,240,293,366,380/Binding site: carbohydrate (asn) (covalent) #status pred

Query Match 51.4%; Score 2403; DB 1; Length 890;
Best Local Similarity 96.1%; Pred. No. 2.9e-113;

Matches 467; Conservative 4; Mismatches 15; Indels 0; Gaps 0;

QY 382 FSDMDADSTFVVOQNSNPAMRAMVPVGLVLTALVTAALALILLRKRKRETFGQAF 441
 DB 405 WSOPLVYSSHDRAGQGGPHSRSTSMVPVGLVLTALVTAALALILLRKRKRETFGQAF 464
 QY 442 DSVARKEPAVHFRAARSPFRERPERIEATLDSIGISDELKEKEDVLIPEQOFTLGRML 501
 DB 465 DSVARKEPAVHFRAARSPFRERPERIEATLDSIGISDELKEKEDVLIPEQOFTLGRML 524
 QY 502 GKGEFGSVREAOIKQEDGSFVKVAVKMLKADIIASSDIEEFLERAACKKEFDHPHVAKL 561
 DB 525 GKGEFGSVREAOIKQEDGSFVKVAVKMLKADIIASSDIEEFLERAACKKEFDHPHVAKL 584
 QY 562 GVSLSRAKGRPLIPVYILPFKMGDLHAFLASRIGENPNPLQTLIRFWDIACGME 621
 DB 585 GVSLSRAKGRPLIPVYILPFKMGDLHAFLASRIGENPNPLQTLIRFWDIACGME 644
 QY 622 YLSRNFIHDLAARNCMLEDMTCVADFGLSRKITYSGDYRQGCASKLPVKMLALESL 681
 DB 645 YLSRNFIHDLAARNCMLEDMTCVADFGLSRKITYSGDYRQGCASKLPVKMLALESL 704
 QY 682 ADNLTYVOSDVMAFGVTMEINTRGOTPYAGIENAEIYNVILGNNLKQPECEMEDVYDL 741
 DB 705 ADNLTYVOSDVMAFGVTMEINTRGOTPYAGIENAEIYNVILGNNLKQPECEMEDVYDL 764
 QY 742 MYQCSADPKORPSTFCIRMELENILGOLSVLASODPLYINIERAEEPTAGSLELPGR 801
 DB 765 MYQCSADPKORPSTFCIRMELENILGOLSVLASODPLYINIERAEEPTAGSLELPGR 824
 QY 802 DOPYSGAGDGSOMGAVGTPSDCRITLTPGGLAEPQGAHQEPSPLENTORLLILLOGL 861
 DB 825 DOPYSGAGDGSOMGAVGTPSDCRITLTPGGLAEPQGAHQEPSPLENTORLLILLOGL 884
 QY 862 LPHSSC 867
 DB 885 LPHSSC 890

RESULT 2
 138912
 receptor tyrosine kinase - human
 C:Species: Homo sapiens (man)
 C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 18-Jun-1999
 C:Accession: J38912
 R:Crossier, K.E.; Hall, L.R.; Lewis, P.M.; Morris, C.M.; Wood, C.R.; Morris, J.C.; Crossier
 Growth Factors 11, 137-144, 1994
 A:Title: Isolation and characterization of the human DTK receptor tyrosine kinase.
 A:Reference number: 138912; MUID:95161080
 A:Accession: J38912
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-882 <RES>
 A:Cross-references: EMBL:U018934; NID:9622984; PIDN:AAC50070.1; PID:9622985
 A:Genetics:
 A:Gene: DTK
 C:Superfamily: protein-tyrosine kinase ax1; fibronectin type III repeat homology; immuno
 F:508-785/Domain: protein kinase homology <KIN>

Query Match 51.3%; Score 2399; DB 2; Length 882;
 Best Local Similarity 95.9%; Pred. No. 4.5e-113;
 Matches 466; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY 382 FSDMDADSTFVVOQNSNPAMRAMVPVGLVLTALVTAALALILLRKRKRETFGQAF 441
 DB 397 WSOPLVYSSHDRAGQGGPHSRSTSMVPVGLVLTALVTAALALILLRKRKRETFGQAF 456
 QY 442 DSVARKEPAVHFRAARSPFRERPERIEATLDSIGISDELKEKEDVLIPEQOFTLGRML 501
 DB 457 DSVARKEPAVHFRAARSPFRERPERIEATLDSIGISDELKEKEDVLIPEQOFTLGRML 516
 QY 502 GKGEFGSVREAOIKQEDGSFVKVAVKMLKADIIASSDIEEFLERAACKKEFDHPHVAKL 561

DB 517 GKGEFGSVREAOIKQEDGSFVKVAVKMLKADIIASSDIEEFLERAACKKEFDHPHVAKL 576
 QY 562 GVSLSRAKGRPLIPVYILPFKMGDLHAFLASRIGENPNPLQTLIRFWDIACGME 621
 DB 577 GVSLSRAKGRPLIPVYILPFKMGDLHAFLASRIGENPNPLQTLIRFWDIACGME 636
 QY 622 YLSRNFIHDLAARNCMLEDMTCVADFGLSRKITYSGDYRQGCASKLPVKMLALESL 681
 DB 637 YLSRNFIHDLAARNCMLEDMTCVADFGLSRKITYSGDYRQGCASKLPVKMLALESL 696
 QY 662 ADNLTYVOSDVMAFGVTMEINTRGOTPYAGIENAEIYNVILGNNLKQPECEMEDVYDL 741
 DB 697 ADNLTYVOSDVMAFGVTMEINTRGOTPYAGIENAEIYNVILGNNLKQPECEMEDVYDL 756
 QY 742 MYQCSADPKORPSTFCIRMELENILGOLSVLASODPLYINIERAEEPTAGSLELPGR 801
 DB 757 MYQCSADPKORPSTFCIRMELENILGOLSVLASODPLYINIERAEEPTAGSLELPGR 816
 QY 802 DOPYSGAGDGSOMGAVGTPSDCRITLTPGGLAEPQGAHQEPSPLENTORLLILLOGL 861
 DB 817 DOPYSGAGDGSOMGAVGTPSDCRITLTPGGLAEPQGAHQEPSPLENTORLLILLOGL 876
 QY 862 LPHSSC 867
 DB 877 LPHSSC 882

RESULT 3
 138412
 receptor tyrosine kinase - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 18-Jun-1999
 C:Accession: J38412
 R:Del, W.; Pan, H.; Hamdy, H.; Gupta, S.L.; Murphy, M.J.
 Oncogene 9, 975-979, 1994
 A:Title: Molecular cloning of a novel receptor tyrosine kinase, tlf, highly expressed
 A:Reference number: 138412; MUID:94151024
 A:Accession: J38412
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-723 <RES>
 A:Cross-references: EMBL:U02556; NID:9467817; PIDN:AAA17407.1; PID:9467818
 C:Superfamily: protein-tyrosine kinase ax1; fibronectin type III repeat homology; imm
 F:331-606/Domain: protein kinase homology <KIN>

Query Match 50.0%; Score 2337.5; DB 2; Length 723;
 Best Local Similarity 92.9%; Pred. No. 4.4e-110;
 Matches 461; Conservative 7; Mismatches 25; Indels 3; Gaps 3;

QY 382 FSDMDADSTFVVOQNSNPAMRAMVPVGLVLTALVTAALALILLRKRKRETFGQAF 441
 DB 220 WSOPLVYSSHDRAGQGGPHSRSTSMVPVGLVLTALVTAALALILLRKRKRETFGQAF 279
 QY 442 DSVARKEPAVHFRAARSPFRERPERIEATLDSIGISDELKEKEDVLIPEQOFTLGRML 501
 DB 280 DSVARKEPAVHFRAARSPFRERPERIEATLDSIGISDELKEKEDVLIPEQOFTLGRML 339
 QY 502 GKGEFGSVREAOIKQEDGSFVKVAVKMLKADIIASSDIEEFLERAACKKEFDHPHVAKL 561
 DB 340 GKGEFGSVREAOIKQEDGSFVKVAVKMLKADIIASSDIEEFLERAACKKEFDHPHVAKL 399
 QY 562 GVSLSRAKGRPLIPVYILPFKMGDLHAFLASRIGENPNPLQTLIRFWDIACGME 621
 DB 400 GVSLSRAKGRPLIPVYILPFKMGDLHAFLASRIGENPNPLQTLIRFWDIACGME 458
 QY 622 YLSRNFIHDLAARNCMLEDMTCVADFGLSRKITYSGDYRQGCASKLPVKMLALESL 681
 DB 459 YLSRNFIHDLAARNCMLEDMTCVADFGLSRKITYSGDYRQGCASKLPVKMLALESL 518
 QY 682 ADNLTYVOSDVMAFGVTMEINTRGOTPYAGIENAEIYNVILGNNLKQPECEMEDVYDL 741

Db 519 ADNLTYQSDVWAFGVTWMEIMTRGQTPYAGIENAEIYNVLIGN-LKQPECMEDVYL 577

QY 742 MYOCMSADPKORPSFTCLRMELLENILGOLSVLASODPLYINIERAEPTAGSGLELPGR 801

Db 578 MYOCMSADPKORPSFTCLRMELLENILGOLSVLASODPLYINIERAEPTAGSGLELPGR 637

QY 802 DQRYSGAGDGGSGMGAVGTPSDCRYILTPGGLAEPQGAHQEPSPLENTORLLLOOGL 861

Db 638 DQRYSGAGDGGSGMGAVGTPSDCRYILTPGGLAEPQGAHQEPSPLENTORLLLOOGL 697

QY 862 LPHSSCADSLKNAKP 877

Db 698 L-HTVAVSPQERASGP 712

RESULT 4

JC4166

protein-tyrosine kinase (EC 2.7.1.112) tyros3 precursor - rat

Alternate names: protein-tyrosine kinase sky; receptor-type tyrosine kinase rse

Species: Rattus norvegicus (Norway rat)

Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: J04166; P0185

R:Ohashi, K.; Honda, S.; Ichihomiya, N.; Nakamura, T.; Mizuno, K.

J. Biochem. 117, 1267-1275, 1995

A:Title: Molecular cloning and in situ localization in the brain of rat sky receptor ty

A:Reference number: J04166; MUID:96104999

A:Molecule type: J04166

A:Molecule type: mRNA

A:Residues: 1-880 <OH>

A:Cross-references: DDBJ:D37880; NID:g1498195; PIDN:BA07119.1; PID:d1007696; PID:g82905

A:Experimental source: brain

A>Note: It is uncertain whether Met-1 or Met-7 is the initiator

R:Lat, C.; Lemke, G.

Neuron 6, 691-704, 1991

A:Title: An extended family of protein-tyrosine kinase genes differentially expressed in

A:Reference number: P0185; MUID:91222560

A:Accession: P0185

A:Molecule type: mRNA

A:Residues: 650-703 <LA1>

A:Experimental source: sciatic nerve

C:Comment: This receptor plays an important role in development, function, and maintain

C:Genetics:

A:Gene: tyro-3

C:Superfamily: protein-tyrosine kinase axl; fibronectin type III repeat homology; immun

C:Keywords: ATP; glycoprotein; growth factor receptor; phosphotransferase; transforming

F:1-31/Domains: (or 7-31) signal sequence #status Predicted <SIG>

F:32-880/Product: (or 32-874) protein-tyrosine kinase tyros3 #status predicted <MAT>

0-109/Domains: immunoglobulin homology <IMM1>

F:146-195/Domains: immunoglobulin homology <IMM2>

F:214-299/Domains: fibronectin type III repeat homology <FN3>

F:312-395/Domains: fibronectin type III repeat homology <FN3B>

F:419-441/Domains: transmembrane #status predicted <TM>

F:506-783/Domains: protein kinase homology <KIN>

F:514-522/Region: protein kinase ATP-binding motif

F:515-766/Domains: cytoplasmic tyrosine kinase #status predicted <CTK>

F:533,753,181,220,230,283,356,370/Binding site: carbohydrate (Aan) (covalent) #status pred

Query Match 48.3%; Score 2257; DB 1; Length 880;

Best Local Similarity 90.3%; Pred. No. 5,7e-106;

Matches 439; Conservative 12; Mismatches 35; Indels 0; Gaps 0;

QY 382 FSDQADSTFVSVOQNSNPAMRAWPVVIGVLTALYAAALAILLRKRRKRTFGQAF 441

Db 395 MSQPLVSSHSHAGQGPPHSTSWPVVGLTALTAALAILLRKRRKRTFGQAF 454

QY 442 DSVARGPAPVAFRAARSPFRERIENTLDSLGISDELKRELVILPEQOFTLRNL 501

Db 455 DSVARGPAPVAFRAARSPFRERIENTLDSLGISDELKRELVILPEQOFTLRNL 514

QY 502 GKGGGSGREAOIKREDGDFVAVKMLKADIIASSDIEEFLREAAKKEEDHPVAKLV 561

Db 515 GKGGGSGREAOIKREDGDFVAVKMLKADIIASSDIEEFLREAAKKEEDHPVAKLV 574

QY 562 GVALRSRAKRLPIPVAILPFKMGDLHAFLLASRIGENFNLPLQTLIRFWDIACGNE 621

Db 575 GVALRSRAKRLPIPVAILPFKMGDLHAFLLASRIGENFNLPLQTLIRFWDIACGNE 634

QY 622 YLSRNFIHDLAARNCMAEDTVCVADPGLSRKITYSDDYRQGCASLPRKWLALBSL 681

Db 635 YLSRNFIHDLAARNCMAEDTVCVADPGLSRKITYSDDYRQGCASLPRKWLALBSL 694

QY 682 ADNLTYQSDVWAFGVTWMEIMTRGQTPYAGIENAEIYNVLIGNRLKQPECMEDVYL 741

Db 695 ADNLTYQSDVWAFGVTWMEIMTRGQTPYAGIENAEIYNVLIGNRLKQPECMEDVYL 754

QY 742 MYOCMSADPKORPSFTCLRMELLENILGOLSVLASODPLYINIERAEPTAGSGLELPGR 801

Db 755 MYOCMSADPKORPSFTCLRMELLENILGOLSVLASODPLYINIERAGPQAEHSPLELPG 814

QY 802 DQRYSGAGDGGSGMGAVGTPSDCRYILTPGGLAEPQGAHQEPSPLENTORLLLOOGL 861

Db 815 DQRYSGAGDGGSGMGAVGTPSDCRYILTPGGLAEPQGAHQEPSPLENTORLLLOOGL 874

QY 862 LPHSSC 867

Db 875 LPHSSC 880

RESULT 5

B53743

protein-tyrosine kinase (EC 2.7.1.112) tyros3 precursor - mouse

N:Alternate names: protein-tyrosine kinase sky; receptor-type tyrosine kinase rse; ty

C:Species: Mus musculus (house mouse)

C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 18-Jun-1999

C:Accession: B53743; S44141; J02146; I49198; I49151; I48863; I48860

R:Mark, M.R.; Scadden, D.T.; Wang, Z.; Gu, Q.; Goddard, A.; Godowski, P.J.

J. Biol. Chem. 269, 10720-10728, 1994

A:Title: rse, a novel receptor-type tyrosine kinase with homology to Axl/Vfo, is expr

A:Reference number: A53743; MUID:94193774

A:Accession: B53743

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-880 <MAR>

A:Cross-references: GB:005683; NID:g469518; PIDN:AAA19237.1; PID:g469519

R:Lat, C.; Gore, M.; Lemke, G.

submitted to the EMBL Data Library, March 1994

A:Description: Structure, expression and activity of TYR03.

A:Reference number: S44141

A:Accession: S44141

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 7-629, 'R', 631-810, 'V', 812-880 <LA1>

A:Cross-references: EMBL:X78109; NID:g473096; PIDN:CAA54995.1; PID:g473097

R:Polvi, A.; Armstrong, E.; Lat, C.; Lemke, G.; Huebner, K.; Spitt, R.A.; Gulda, L.C

Gene 134, 289-293, 1993

A:Title: The human TYR03 gene and pseudogene are located in chromosome 15q14-q25.

A:Reference number: J02145; MUID:94085793

A:Accession: J02145

A:Residues: 509-629, 'R', 631-647, 'P', 649-780 <POL>

R:Crosier, P.S.; Lewis, P.M.; Hall, L.R.; Vitas, M.R.; Morris, C.M.; Beler, D.R.; Woo

Growth Factors 11, 125-136, 1994

A:Title: Isolation of a receptor tyrosine kinase (DTK) from embryonic stem cells: str

A:Reference number: I49198; MUID:95161079

A:Accession: I49198

A:Status: preliminary;

A:Molecule type: translated from GB/EMBL/DBDB

A:Residues: 1-880 <RES>

A:Cross-references: EMBL:U18933; NID:g622982; PIDN:AAC52148.1; PID:g622983

R:Schulz, N.T.; Pauliac, C.I.; Lee, L.; Zhou, R.

Brain Res. Mol. Brain Res. 28, 273-280, 1995

A:Title: Isolation and expression analysis of tyros3, a murine growth factor receptor

A:Reference number: I49151; MUID:95240399

A:Accession: I49151

A:Status: nucleic acid sequence not shown; translated from GB/EMBL/DBDB

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A:Molecule type: mRNA
A:Residues: 7-880 <RE2>
A:Cross-references: EMBL:U18342; NID:9687625; PIDN:AAB26942.1; PID:9687626
R:Biesecker, L.G.; Gianmola, D.M.; Emerson, S.G.
Oncogene 10, 2239-2242, 1995
A>Title: Identification of alternative exons, including a novel exon, in the tyrosine kinase gene
A:Reference number: I48861; MUID:95303487
A:Accession: I48861
A>Status: preliminary; translated from GB/EMBL/DDBT
A:Molecule type: DNA
A:Residues: 1-92 <RE3>
A:Cross-references: EMBL:U23721; NID:9901992; PIDN:AAC52217.1; PID:9901996
R:Lat, C.; Gore, M.; Lemke, G.
Oncogene 9, 2567-2578, 1994
A>Title: Structure, expression, and activity of Tyro 3, a neural adhesion-related receptor
A:Reference number: I48860; MUID:94336210
A:Accession: I48860
A>Status: preliminary; translated from GB/EMBL/DDBT
A:Molecule type: mRNA
A:Residues: 7-629,'R','631-810','V','812-880 <RE4>
Oss-references: EMBL:X78103; NID:9473096; PIDN:CMA54995.1; PID:9473097
A:Gene: tyroz; Dtk: Etk2/Tyroz
A:Introns: 32/1
C:Superfamily: protein-tyrosine kinase ax1; fibronectin type III repeat homology; Immunoglobulin fold
C:keywords: ATP; glycoprotein; growth factor receptor; phosphotransferase; transforming
F:1-31/Domian: (or 7-31) signal sequence #status predicted <SIG>
F:32-880/Product: protein-tyrosine kinase tyroz #status predicted <AT>
F:50-109/Domian: immunoglobulin homology <IMM1>
F:146-195/Domian: immunoglobulin homology <IMM2>
F:214-299/Domian: fibronectin type III repeat homology <FN3A>
F:312-395/Domian: fibronectin type III repeat homology <FN3B>
F:419-441/Domian: transmembrane #status predicted <TM>
F:506-763/Domian: protein kinase homology <KIN>
F:514-522/Region: protein kinase ATP-binding motif
F:515-766/Domian: cytoplasmic tyrosine kinase #status predicted <CTR>
F:53,75,181,220,230,283,356,370/Binding site: carbohydrate (asn) (covalent) #status predicted
Query Match 48.0%; Score 2246; DB 2; Length 880;
Best Local Similarity 90.1%; Pred. No. 2e-105;
Matches 438; Conservative 14; Mismatches 34; Indels 0; Gaps 0;
QY 382.FSQMDADTSFYVOQNPNPRAWVPVGLVALVTAAALAILKKRRKTRFGQAF 441
DB 395.WSOPLVVSSHAGCGPPHSRTSWPVVLGVLTALTALTAALAILKKRKKEFRFGQAF 454
QY 442.DSVARGPAPVHFAAREBFNERPRERITATDSGISSELKEKEDVLIPEOQTTLGRML 501
DB 455.DSVARGPAPVHFAAREBFNERPRERITATDSGISSELKEKEDVLIPEOQTTLGRML 514
QY 502.GKGEGSYREAQLKOEDSFYKVAVKMLKADIASSDIEELFREAAKKEPDHFHVAKLY 561
DB 515.GKGEYSYREAQLKOEDSFYKVAVKMLKADIASSDIEELFREAAKKEPDHFHVAKLY 574
QY 562.GVSLSRAKRGKLPIPAVTLIPPKHGDLHAFTLASRIGENPNPLQLQTLIRFMYDIAGME 621
DB 575.GVSLRSRAKRGKLPIPAVTLIPPKHGDLHAFTLASRIGENPNPLQLQTLIRFMYDIAGME 634
QY 622.YLSSRNFIHRRLAARNCLAEADMTVCVADFGLSKRIISGDIYRGGCAKSLPYKYLALDSL 681
DB 635.YLSSRNFIHRRLAARNCLAEADMTVCVADFGLSKRIISGDIYRGGCAKSLPYKYLALDSL 694
QY 682.ADNITYVOSDVMAEAVTMMELINTRGOTPYAGIENAEITYNYLIGNRKAKOPPECDEHYDL 741
DB 695.ADNITYVSHVDVMAEAVTMMELINTRGOTPYAGIENAEITYNYLIGNRKAKOPPECDEHYDL 754
QY 742.MYCWSADPKRPBPFTCLRMLENLICQLSYLSASODPLYINIERAPEPTAGSGLELPGR 801
DB 755.MYCWSADPKRPBPFTCLRMLENLICQLSYLSASODPLYINIERAPEPTAGSGLELPGR 814
QY 802.DQPSGAGDGGMGVNGSTPDCRYLLTPGGLAQPOGAHQEPSPINTEORILLILQOG 861

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QY	862	LPHSSC	867	
Db	875	LPHSSC	880	
RESULT	6			
	149152			
	protein-tyrosine kinase (EC 2.7.1.112) tyro3, isoform B - mouse			
	Alt: alternate names: tyrosine kinase growth factor receptor			
	C:Species: Mus musculus (house mouse)			
	C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999			
	C:Accession: I49152; I48861			
	R:Schulz, N.T.; Paulhac, C.I.; Lee, L.; Zhou, R.			
	Brain Res. Mol. Brain Res. 28, 273-280, 1995			
	A:Title: Isolation and expression analysis of tyro3, a murine growth factor receptor			
	A:Reference number: I49151; MUID:95240399			
	A:Accession: I49152			
	A:Status: preliminary; translated from GB/EMBL/DBJ			
	A:Molecule type: mRNA			
	A:Residues: 1-876 <RES>			
	A:CROSS-references: EMBL:U01343; NID:9687627; PIDN:AA26943.1; PID:9687628			
	R:Biesecker, L.G.; Giamola, D.M.; Emerson, S.G.			
	Oncogene 10, 2239-2242, 1995			
	A:Title: Identification of alternative exons, including a novel exon, in the tyrosine			
	A:Reference number: I48861; MUID:95304867			
	A:Accession: I48861			
	A:Status: preliminary; translated from GB/EMBL/DBJ			
	A:Molecule type: DNA			
	A:Residues: 1-88 <RES>			
	A:CROSS-references: EMBL:U23721; NID:9901992; PIDN:AAC52215.1; PID:9901994			
	C:Genetics:			
	A:Gene: tyro3; Etk2/tyro3			
	A:Introns: 28/1			
	C:Superfamily: protein-tyrosine kinase axl, fibronectin type III repeat homology; Imm			
	C:Keywords: ATP; glycoprotein; growth factor receptor; phosphotransferase			
	E:43-105/Domain: Immunoglobulin homology <IMM>			
	F:502-779/Domain: protein kinase homology <KIN>			
	F:510-518/Region: protein kinase ATP-binding motif			
Query Match	48.08;	Score 2246;	DB 2;	Length 876;
Best Local Similarity	90.18;	Pred. No. 2e-105;		
Matches 438;	Conservative 14;	Mismatches 34;	Indels 0;	Gaps 0;
QY	382	FSQOMADSTFVVOQONSNPAMRANVPVGLVATYTAALAILLRKRKRTRFGQAF	441	
Db	391	WSQPLVYSSHHAGRGQPPHSRTSMVPVGLVATYTAALAILLRKRKRTRFGQAF	450	
QY	442	DSVARGEPAVHFRARNSFRERPERIEATLDSIGISDELKEKEDVLIPEOGFTLRML	501	
Db	451	DSVARGEPAVHFRARNSFRERPERIEATLDSIGISDELKEKEDVLIPEOGFTLRML	510	
QY	502	GKGGEGSREOLQOEQSGSFYKAVYKMLKADITASSSIEEFLRPAACMKEDPHRAKLV	561	
Db	511	GKGGEGSREOLQOEQSGSFYKAVYKMLKADITASSSIEEFLRPAACMKEDPHRAKLV	570	
QY	562	GVSLSRAKGRPLPIPVYILPFMKHGDHAFLLASRIENFNPILPLOTILFPMVDIAGME	621	
Db	571	GVSLSRAKGRPLPIPVYILPFMKHGDHAFLLASRIENFNPILPLOTILFPMVDIAGME	630	
QY	622	YLSSRNFIHDLAARNCMLEDMTVCVADFGLSKRIYSGDYRQGCASKLPVKMLALESL	681	
Db	631	YLSSRNFIHDLAARNCMLEDMTVCVADFGLSKRIYSGDYRQGCASKLPVKMLALESL	690	
QY	682	ADNLYTVQSDVMAAGVYVMEINTRGOTFYAGIEAEATYNTLLIGNRLKOPPECMEDVYDL	741	
Db	691	ADNLYTVQSDVMAAGVYVMEINTRGOTFYAGIEAEATYNTLLIGNRLKOPPECMEDVYDL	750	
QY	742	MYQWMSADPKQORSFTCLRLMELENTIGQLSVLSASODPLYINIERAEPTAGSLLEPGR	801	
Db	751	MYQWMSADPKQORSFTCLRLMELENTIGQLSVLSASODPLYINIERAEPTAGSLLEPGR	810	

QY 802 DQPSGAGDGGMGAVGTPSPDCRRILRPGGLAEQPGAEHPESPFLNWTQRLLLQGL 861
 Db 811 ERSSSEAGDGGGAVGIPSDSRITFPGGLSESPGLEQPEPFLNENRLLQGL 870
 QY 862 LPHSSC 867
 Db 871 LPHSSC 876

RESULT 7
 I58411
 protein-tyrosine kinase (EC 2.7.1.112) bcr - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 18-Jun-1999
 C:Accession: I58411
 R:Fujimoto, J.; Yamamoto, T.
 Oncogene 9, 693-698, 1994
 .Title: bcr, a mouse gene encoding a novel receptor-tyrosine kinase, is pr
 Reference number: I58411; MUID:94150990
 .Accession: I58411
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-856 <RES>
 C:Cross-references: GB:D17393; NID:9801867; PID:BA04216.1; PID:9801868
 C:Superfamily: protein-tyrosine kinase axl; fibronectin type III repeat homology; immun
 C:Keywords: ATP; glycoprotein; phosphotransferase
 F:501-778/Domain: protein kinase homology <Kin>
 F:509-511/Region: protein kinase ATP-binding motif

Query Match 44.58; Score 2080; DB 2; Length 856;
 Best Local Similarity 87.78; Pred. No. 3.9e-97;
 Matches 408; Conservative 15; Mismatches 40; Indels 2; Gaps 1;

QY 382 FSQDWDSTFVVOQNSNPMRAVVPVGLVLTALVTAALAILLRKRKRKREPGQAF 441
 Db 390 WSGPLVYSSHDHNGRQPPRSKTSRYVYGLVLTALVTAALAILLRKRKRKREPGQAF 449
 QY 442 DSYMARGEPAVHFAARSFNRPERIEATLDSIGISDEKEKEDVLIPEQOFTLGRML 501
 Db 450 DSYMARGEPAVHFAARSFNRPERIEATLDSIGISDEKEKEDVLIPEQOFTLGRML 509
 QY 502 GKEEFSVRAQAKOEGSGVKAAYKMLKADITLASSDIEEFLKFAACKEFDHPHAKLV 561
 Db 510 GKEEFSVRAQAKOEGSGVKAAYKMLKADITLASSDIEEFLKFAACKEFDHPHAKLV 569
 QY 562 GVALRSRAKRLPIPMVILPFMKHGDHAFLLASRIGENFNPILQTLIRPMVDIAGME 621
 Db 570 GVALRSRAKRLPIPMVILPFMKHGDHAFLLASRIGENFNPILQTLIRPMVDIAGME 629
 QY 622 YLSSRNFIHDLAARNCMAEDMTVCVADFGLSRKITYSGDYRQGCASKLPVWLALESL 681
 Db 630 YLSSRNFIHDLAARNCMAEDMTVCVADFGLSRKITYSGDYRQGCASKLPVWLALESL 689
 QY 682 ADNLTVQVGVYVAFGTVMETIRGCTPRVAGINAEIYNTLIGNRLKOPPECEMEDVYL 741
 Db 690 ADNLTVQVGVYVAFGTVMETIRGCTPRVAGINAEIYNTLIGNRLKOPPECEMEDVYL 749
 QY 742 MYOCMSADPKQSPFCYCLRELENIIGOLSVLASODPLCINIERKEEPNAGSLPEGR 801
 Db 750 MYOCMSADPKQSPFCYCLRELENIIGOLSVLASODPLCINIERKEEPNAGSLPEGR 809
 QY 802 DQPSGAGDGGMGAVGTPSPDCRRILRPGGLAEQPGAEHPESPFLNWTQRLLLQGL 844
 Db 810 ERSSSEAGDGGGAVGIPSDSRITFPGGLSESPGLEQPEPFLNENRLLQGL 854

RESULT 8
 JE0082
 GPI-linked receptor precursor - mouse
 N:Alternate names: GFRalpha-3
 C:Species: Mus musculus (house mouse)

C>Date: 21-May-1998 #sequence_revision 29-May-1998 #text_change 17-Mar-1999
 C:Accession: JE0082
 R:Nomoto, S.; Ito, S.; Yang, L.X.; Kiuchi, K.
 Biochem. Biophys. Res. Commun. 244, 849-853, 1998
 .Title: Molecular cloning and expression analysis of GFRalpha-3, a novel cDNA related
 A:Reference number: JE0082; MUID:98205811
 A:Accession: JE0082
 A:Molecule type: mRNA
 A:Residues: 1-397 <NOM>
 A:Cross-references: DDBJ:AB008833; NID:92627159; PID:92627160
 C:Comments: This protein plays a distinct role in cell survival and differentiation.
 C:Keywords: glycoprotein
 F:1-25/Domain: signal sequence
 F:380-397/Region: hydrophobic
 F:92,145,306/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 40.28; Score 1880; DB 2; Length 397;
 Best Local Similarity 94.18; Pred. No. 1.8e-87;
 Matches 354; Conservative 5; Mismatches 11; Indels 6; Gaps 1;

QY 54 LEAGNSLATENREYNSTQTKRRCPEANPCKAYOHLGCTSSLSRPLLEESAMADCL 113
 Db 25 LGAGNSLATENREYNSTQTKRRCPEANPCKAYOHLGCTSSLSRPLLEESAMADCL 84
 QY 114 EAAEOLRNSSLIDCRCHRRKHQATCLDIYTWVHPARSGDYELDVPEDYTSKPMK 173
 Db 85 EAAEOLRNSSLIDCRCHRRKHQATCLDIYTWVHPARSGDYELDVPEDYTSKPMK 144
 QY 174 NLSKLNKAFPSDLCKFAMLCITLHDKCDRLRRAYGEAGSGIRCORHLCLAQLRSEFEKA 233
 Db 145 NLSKLNKAFPSDLCKFAMLCITLHDKCDRLRRAYGEAGSGIRCORHLCLAQLRSEFEKA 204
 QY 234 AESHAGGLICPPPPDAGCGERRNTIAPSCALPSYTRNCIDLRSCPADLCSRLMD 293
 Db 205 AESHAGGLICPPPPDAGCGERRNTIAPSCALPSYTRNCIDLRSCPADLCSRLMD 264
 QY 294 FQTHCHPMDILGTCATGOSRCLRAYLGLTAMTPFISKVNTVYALSTCGSGSLMD 353
 Db 265 FQTHCHPMDILGTCATGOSRCLRAYLGLTAMTPFISKVNTVYALSTCGSGSLMD 324
 QY 354 CEOLERSFQNPCLVPAIAKMFHRLQFSQDMADSTFVVOQNSNPMALR-----LQP 378
 Db 325 CEOLERSFQNPCLVPAIAKMFHRLQFSQDMADSTFVVOQNSNPMALR-----LQP 378
 QY 414 LFLVYRAALALILR 429
 Db 379 RLPLSFSLPILLD 394

RESULT 9
 A41527
 protein-tyrosine kinase (EC 2.7.1.112) axl precursor, major splice form - human
 N:Alternate names: transforming protein axl; ufo receptor
 C:Species: Homo sapiens (man)
 C>Date: 28-May-1992 #sequence_revision 05-Jan-1996 #text_change 16-Jul-1999
 C:Accession: A41527; B38269; J39203; G02782
 R:O'Bryan, J.P.; Fyfe, R.A.; Cogswell, P.C.; Neuberger, A.; Kitch, B.; Prokop, C.; Esp
 Mol. Cell. Biol. 11, 5016-5031, 1991
 .Title: axl, a transforming gene isolated from primary human myeloid leukemia cells,
 A:Reference number: A41527; MUID:92017777
 A:Accession: A41527
 A:Molecule type: mRNA
 A:Residues: 1-894 <OAB>
 A:Cross-references: GB:M76125
 A:Experimental source: axl(+)
 A:Accession: B41527
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-337, 'K', 339-428, 438-894 <OAB>
 A:Cross-references: GB:M76125; NID:9292869; PID:AAA61243.1; PID:9292870
 A:Experimental source: axl(-)
 A>Note: the authors translated the codon AAG for residue 338 as Leu

A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-302, 'P', 304-429, 'E', 431-638, 'G', 640-894 <MT>
A:Cross-references: EMBL:X57019; NID:937592; PIDN:CAA0338.1; PID:q37593
C:Comment: This protein is overexpressed in chronic myelogenous leukemia and induces neoplasia
C:Genetics:
A:Gene: GDB:AXL; UFO
A:Cross-references: GDB:133764; OMIM:109135
A:Map position: 19q13.1-19q13.1
C:Function:
A:Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C:Superfamily: protein-tyrosine kinase xtl; fibronectin type III repeat homology; Immunoglobulin fold
C:Keywords: alternative splicing; ATP; duplication; glycoprotein; Leukemia; magnesium; P
tein kinase
F:1-32/Domain: signal sequence #status predicted <SIG>
F:33-894/Product: protein-tyrosine kinase xtl, major splice form #status predicted <MA>
F:49-119/Domain: immunoglobulin homology <IM1>
F:153-307/Domain: immunoglobulin homology <IM2>
F:224-320/Domain: fibronectin type III repeat homology <FN3A>
F:333-417/Domain: fibronectin type III repeat homology <FN3B>
F:448-472/Domain: transmembrane #status predicted <TM>
F:534-810/Domain: protein kinase homology <KIN>
F:542-550/Region: protein kinase ATP-binding motif
F:44,157,198,339,345,401/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:567,585,672/Active site: Lys, Glu, Asp #status predicted
F:677,690/Binding site: magnesium (Asn, Asp) #status predicted
*03/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
*/79,821/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted

RESULT 10
523065
ufo protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-Feb-1994 #sequence_revision 01-Sep-1995 #text_change 16-Jul-1999
C:Accession: 523065
R:Faust, M.; Ebensperger, C.; Schulz, A.S.; Schleithoff, L.; Hamelster, H.; Barttram, Oncogene 7, 1287-1293, 1992
A:Title: The murine ufo receptor: molecular cloning, chromosome localization and in
A:Reference number: S23065; M01D:9231953/
A:Accession: 523065
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-888 <FAU>
A:Cross-references: EMBL:X63535; NID:g55121; PIDN:CAA45097.1; PID:g55122
C:Genetic: ufo
A:Gene: ufo
C:Superfamily: protein-tyrosine kinase axl; fibronectin type III repeat homology; imm
C:Keywords: ATP; autophosphorylation; phosphoprotein; transmembrane protein
E:43-113/Domain: immunoglobulin homology <IMM>
E:528-804/Domain: protein kinase homology <KIN>
F:536-544/Region: protein kinase ATP-binding motif

Query Match	25.2%	Score 1178.5	DB 2	Length 888
Best Local Similarity	51.3%	Pred. No. 4.7e-52		
Matches 237	Conservative 69	Mismatches 129	Indels 27	Gaps 6
QY	399	SNPAMRA----	WPPVVLGVLTATVATAAALILILKKRKETREFOAQDSVANGEPANVF	454
Db	433	SEPPRAFSPMPWTVLLGALVAACVLLILALFVHRBRKKEFRGCEVPEYERSELVYR		492
QY	455	RAARSPERPEREATLDSIGSIDELKELVDYLIREOFTLGRMLKGFEGVGRQAOL	514	
Db	493	KVRKISR--RTEATLNLNGISSEELKEKRLVMDRHHVLAJKTGIDEEFQVVMGOL	549	
QY	515	KOEDGSFVAVVIMLKADIIASSDIEEFLREAAKMEFEDHPRHYAKTVGLSRSAKRLP	574	
Db	550	NQDD-SILTKAAVATMKALITCRSELEDLSEAVCMKEFDHPNWRKLIGVCFQSGDRGFR	608	
QY	575	IPAVIILPFMAHGDLHAFLLASRIGENPENTLPLOTLIREVWDIACGMETLSRNFIRHDLA	634	
Db	609	EPVAVIILPFMAHGDLHSLILTSRLGDQVPELPTMLVAFMADISGMETLSKTRFIHRDLA	668	
QY	635	ARRCMIAEDTYCVADGSLGRKIYSGDYRQOGASRTPVWMLAESTADLYLVQSGVMA	694	
Db	669	ARRCMINENNSVADPGLSKKIYNGDIYRQGRILAKPAPVMIIESIADAVYTSKSDVMS	728	
QY	695	FGVLTMEIMTRGOTPYAGIENAEIYNTLIGGNRLKOPPECEMEDVYDILMYQMSADPRORP	754	
Db	729	FGVLTMEIATRGOTPYRGVENSEIYDLRQGNRLKOPVDPLDGLYSLMSRCWELNPRDR	788	
QY	755	SFTCLMELENITIGOLSVLSASODPLYINIERA-----EETIAGSGLELPRORDPYSGAGD	810	
Db	789	SFTLELDEDLNTKALPPRADOEPDEILTVNMDGEGSHLEPRGAAGADPTQPPD----	844	
QY	811	GGSGMGAVGGTSDCRYLTPG-----GLADOPGAE	841	

Db 845 SCSCLTADVSHAGRVILCPSTAPGPTLSADRCPCAPPGQED 886

RESULT 11

138547

novel cellular proto-oncogene - human

C:Species: Homo sapiens (man)

C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 18-Jun-1999

C:Accession: 138547

R:Graham, D.K.; Dawson, T.L.; Mullaney, D.L.; Snodgrass, H.R.; Earp, H.S.

Cell Growth Differ. 5, 647-657, 1994

A:Title: Cloning and mRNA expression analysis of a novel human protooncogene, c-mer.

A:Reference number: 138547; MUID:94368701

A:Accession: 138547

A:Status: Preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-999 <GRA>

A:Cross-references: EMBL:U08023; NID:9505664; PIDN:AAB60430.1; PID:9505665

Genetics:

C:Gene: c-mer

C:Superfamily: protein-tyrosine kinase axl; fibronectin type III repeat homology; Immunc

F:585-861/Domain: protein kinase homology <KIN>

Query Match 24.7%; Score 1155.5; DB 2; Length 999;
Best Local Similarity 38.8%; Pred. No. 7.4e-51;

Matches 294; Conservative 115; Mismatches 207; Indels 141; Gaps 27;

233 AAESH-----AGCLL-----CPCPEDAGCGERRNTAPSCALPSV-----TP--N 273

Db 261 SCEAHNDKGLTVSGOVQINIKAIPEPTEVSI-----RNSTASHILISWVGFEDGYSFPRN 316

QY 274 C-LDLRSCRADPLCRSLMDPQCHCHMDLIGTCATQSSRLRAY-----LGILG-TA 325

Db 317 CSTGVK---EADPLANGVMYFNTSALP---HLQIKOLQALANYSIGVSCMDIGMSA 369

QY 326 MTP-----NFISKVNTVAL-----SCTCGSS 347

Db 370 VSPWILASTEGASVAPLANLTVFLNEDSDNDVDMKPRPTQODGELVGRISHVWSA 429

QY 348 GNLODECHQLERSTSQ-----NPLVEALIAAKRHFRLF-----QDMAD-S 389

Db 430 GISKELEEVQONGSFRARISYOVHNATCTVLAATRGVGFSPVKEIFPAHGWVYA 489

QY 390 TFSVYQOONSPPARAWPVVLG-----VLAITYAALALILKRKRRTREGQAF--- 442

Db 490 PSSIPADGNADP-----VLIFGCGFGFILGLILYISA---IKRVOETKFGNAFTEE 541

QY 442 DSVARGEPAVHFAARAFSFRPERPERIATLDSIGISDELKEDVLIIPDQFTLGRL 501

Db 542 DS-----ELVYNYIAKSFGR---RAIELTHSHAGVSELDONKEDVDYIDNLLILGLIL 593

QY 502 GKGFSGYREAOQLKQEDGSFYKVAVKMLKADIASSDIEELREAAKKEFDHPHYATLY 561

Db 594 GEGFSGYMEGNLKEOEGTSLKVAVKTKLNDNSHREIEELSEAAKCKDPSHNVITLL 653

QY 562 GVSLSRAKGRLPDPVITLPRKMGDLAFLAISRIGENPNPLQTIIRAVDIACME 621

Db 654 GVCLEMSSQG-IPKAVYILPRKMGDLAFLAISRIGENPNPLQTIIRAVDIACME 712

QY 622 YLSRNFIRHDLAARNCLMADMTVCVADFGLSRKRIYSGDYRROGCAKSLPVKMLALESL 681

Db 713 YLSRNFIRHDLAARNCLMADMTVCVADFGLSRKRIYSGDYRROGCAKSLPVKMLALESL 772

QY 682 ADNTYVQSDVMAFGVTMMELIRGOTPYAGIENAIYNYLIGNRKLQPPEDMEDVDL 741

Db 773 ADRTYVQSDVMAFGVTMMELIRGOTPYAGIENAIYNYLIGNRKLQPPEDMEDVDL 832

QY 742 MYOQWMDPQRPQFTCLMLENIIIGOLSVLSASQDPLYN---IERAEPTLGGSL-E 797

Db 833 MYOQWMDPQRPQFTCLMLENIIIGOLSVLSASQDPLYN---IERAEPTLGGSL-E 892

QY 798 LPGRDQPYSGAGDGSQMGAVG-----GRPSDCRYLLIPGCG-----LAPGQAEHP 844

Db 893 LDNLNDPDSITINACTPRAISVYVAEVDHDSKPHREGRIYILNGSEEMEDLTSAFSAATAE 952

QY 845 ESPLNQTRLL-----LIQGLLPHSSCADASLKNAD 876

Db 953 KNSVLPGERLYANGVSWSHSSMLPLGSSLPDELLEAD 989

RESULT 12

149276

c-mer tyrosine kinase receptor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999

C:Accession: 149276

R:Graham, D.K.; Bowman, G.W.; Dawson, T.L.; Stanford, W.L.; Earp, H.S.; Snodgrass, H.

Oncogene 10, 2349-2359, 1995

A:Title: Cloning and developmental expression analysis of the murine c-mer tyrosine k

A:Reference number: 149276; MUID:95303502

A:Accession: 149276

A:Status: Preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-994 <RES>

A:Cross-references: EMBL:U21301; NID:9885969; PIDN:AA80222.1; PID:9885970

C:Superfamily: protein-tyrosine kinase axl; fibronectin type III repeat homology; Imm

C:Keywords: ATP; receptor

F:580-856/Domain: protein kinase homology axl; fibronectin type III repeat homology; Imm

F:588-596/Region: protein kinase ATP-binding motif

Query Match 24.3%; Score 1137; DB 2; Length 994;
Best Local Similarity 53.2%; Pred. No. 6.2e-50;

Matches 236; Conservative 71; Mismatches 103; Indels 34; Gaps 10;

QY 409 VVLG-----VLAITYAALALILKRKRRTREGQAF---DSVYARGEPAVHFAARAFS 460

Db 499 IILGFCGFIILIGLILCISLA---LRRVQETKFGAFSEDSOL-----VNYRANKSF 550

QY 461 NRPERRIEATLDSIGISDELKEDVLIIPDQFTLGRLMKGEGFSVREAOQLKQEDGS 520

Db 551 CR---RAIELTQSLGVSELDONKEDVDYIDNLLILGLILGILGLILGILGLIL 607

QY 521 FVYAVYKMLKADIASSDIEELREAAKKEFDHPHYAKLVGSLSRANGRLDPVYL 580

Db 608 SOKAVYKMLKADNSOREIEELSEAAKCKDPSHNVITRLIGVCIELSSQG-IPKAVYL 666

QY 581 PFMRGDLHAFILASRIGENPNPLQTIIRAVDIACMEYLSRNFIRHDLAARNCL 640

Db 667 PFMRGDLHAFILASRIGENPNPLQTIIRAVDIACMEYLSRNFIRHDLAARNCL 726

QY 641 AEDMTVCVADFGLSRKRIYSGDYRROGCAKSLPVKMLALESLADNLYVQSDVMAFGVTM 700

Db 727 RDDMTVCVADFGLSKRIYSGDYRROGRIAKMPYKWIASELADRYTSKSDVMAFGVTM 766

QY 701 EIMRGOTPPAGINAIYNYLIGNRKLQPPEDMEDVDLMTQCSADKPQRPSTCLR 760

Db 787 EITRGMTPPPGVQNHMMYVLLHGRHLKQPPEDLDELVDIMKSCWADPLDRPFTSVLR 846

QY 761 MELNIIIGOLSVLSASQDPLYNIERAE---EPTAGSLELPGRD---QPSAGDGSQMG 815

Db 847 LQLEKLESIPDADOKRSITTYINTQLLESCEGIANGP-SLTGLDMNDIPDSITIACTPGA 905

QY 816 AVGTGSDC-----RYILTPG 831

Db 906 AVSVYTALEVHNNLRERYITLNGG 929

RESULT 13

523251

protein-tyrosine kinase (EC 2.7.1.112) ark precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 19-Dec-1997

C:Accession: 523251

R:Rescigno, J.; Mansukhani, A.; Basilio, C.
 Oncogene 6, 1909-1913, 1991
 A:Title: A putative receptor tyrosine kinase with unique structural topology.
 A:Reference number: S23251; MID:92019811
 A:Accession: S23251
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-942 <RES>
 A:Cross-references: EMBL:X59560
 C:Genetics:
 A:Gene: ark
 C:Superfamily: protein-tyrosine kinase axl; fibronectin type III repeat homology; immunoglobulin; ATP; autophosphorylation; glycoprotein; phosphoprotein; phosphotransferase;
 F:1-19/Domain: signal sequence & status predicted <Sig>
 F:20-942/Product: protein-tyrosine kinase ark & status predicted <Kat>
 F:446-466/Domain: transmembrane & status predicted <TM>
 F:528-804/Domain: protein kinase homology <KIN>
 F:536-544/Region: protein kinase ATP-binding motif
 F:151,192,339,395,677/Binding site: carbohydrate (Asn) (covalent) & status predicted

Query Match 24.2% Score 1130.5; DB 2; Length 942;
 Best Local Similarity 57.4%; Pred. No. 1.2e-49;
 Matches 220; Conservative 62; Mismatches 92; Indels 9; Gaps 4;

QY 399 SNPAMRA---WPPVYGVLTALVTAALALILRRRRKRETRFGAOFDSVMAEGEPAVHP 454
 DB 433 SEPPPAFSPWYVYVLLGALVAAACVLIALFLVHRKKETKRGVEFPEPELVARI 492
 QY 455 RAARSRNRRPERIEATLDSIGISDELKEKEDVLIPEOQFTLRMGKGFSGSVRAEOL 514
 DB 493 RVKRSYSR---RTTEATLNSLIGISELKEKRLRVMDRHRVMAAGKTLGSEGEAVAEGL 549
 QY 515 KQDGSFVVAAYMLADITIASDIEEFLREAAKMEFDPHVAIKVGSLSRAKGRIP 574
 DB 550 NQDD-SILVAAYTKIVICTRSELEDFSEAVCKMEFHPNVMRLIGVCFQSGSDREGPP 608
 QY 575 IPWVILPFMKHGLDIAFLASRIGENPFLPLOTILRFWDIACGMEYLSRNFIRDLA 634
 DB 609 EPPVILPFMKHGLDIAFLASRIGENPFLPLOTILRFWDIACGMEYLSRNFIRDLA 668
 QY 635 ARRCMLAEDMTVCVADFGLSRKITYSGDYRQGCASRLPVKWLAEGLADNLTYSQSDVA 694
 DB 669 ARRCMLAEDMTVCVADFGLSRKITYSGDYRQGCASRLPVKWLAEGLADNLTYSQSDVA 728
 QY 695 FGVTMEINTRGOTPYAGIENAEIYVYLGKRLKOPPECMEDVDLMTQCSADPKORP 754
 DB 729 FGVTMEINTRGOTPYAGIENAEIYVYLGKRLKOPPECMEDVDLMTQCSADPKORP 788
 755 SFTCLMELENIIGQLSVLASQ 777
 DB 789 SFAELREDELENTL-KICPLLRQ 810

RESULT 14
 A49714
 protein-tyrosine kinase (EC 2.7.1.112) c-eyk precursor - chicken

C:Species: Gallus gallus (chicken)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A49714
 R:Jia, R.; Hanafusa, H.
 J. Biol. Chem. 269, 1839-1844, 1994
 A:Title: The proto-oncogene of v-eyk (v-ryk) is a novel receptor-type protein tyrosine kinase
 A:Reference number: A49714; MID:94124527
 A:Accession: A49714
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-974 <JIA>
 A:Cross-references: GB:L21719; MID:9438522; PIDN:AAC38010.1; PID:G438522
 C:Superfamily: protein-tyrosine kinase axl; fibronectin type III repeat homology; immunoglobulin; ATP; autophosphorylation; glycoprotein; phosphotransferase; transmembrane protein
 F:575-851/Domain: protein kinase homology <KIN>
 F:583-591/Region: protein kinase ATP-binding motif

Query Match 23.6% Score 1102.5; DB 1; Length 974;
 Best Local Similarity 48.2%; Pred. No. 3.2e-48;
 Matches 235; Conservative 75; Mismatches 141; Indels 37; Gaps 9;

QY 409 VYLGVLTALVTAALAL---ILRRRRKRETRFGAOF---DSVMAEGEPAVHPRAARSENR 462
 DB 494 VALGFVCGTV-AVGLILCLSVIQRCKETKYNFNRDS-----ELVYNTAKRSYCR 547
 QY 463 EPPERIEATLDSIGISDELKEKEDVLIPEOQFTLRMGKGFSGSVRAEOLKQDGSFV 522
 DB 548 ---RAVELLIGSLGVSSSELQKLOVDNRMLSLGKVLGESEFGSGVMEGRISOPEGTQ 604
 QY 523 KVAAYMLKADITIASDIEEFLREAAKMEFDPHVAIKVGSLSRAKGRIPVILPF 582
 DB 605 KVAAYTKMDNSHREIEEFLSEAAKMDFDHPNVIKLLGVCIELSSQ-QIPKPVILPF 663
 QY 583 MKHGLDIAFLASRIGENPFLPLOTILRFWDIACGMEYLSRNFIRDLAARCMLE 642
 DB 664 MKHGLDIAFLASRIGENPFLPLOTILRFWDIACGMEYLSRNFIRDLAARCMLE 723
 QY 643 DMTVCVADFGLSRKITYSGDYRQGCASRLPVKWLAEGLADNLTYSQSDVAEFTVMEI 702
 DB 724 DMTVCVADFGLSRKITYSGDYRQGCASRLPVKWLAEGLADNLTYSQSDVAEFTVMEI 783
 QY 703 MTRGOTPYAGIENAEIYVYLGKRLKOPPECMEDVDLMTQCSADPKORPSTCLME 762
 DB 784 ATRGMPYPGVQNHIEYELFEGRLKRPENCIDELVDIIMSCWRAEPADRTFQGLAVH 843
 QY 763 LENIIGQLSVLASQDPLXINERAE-----PTAGSLELPGRDOPYGA 808
 DB 844 LEKLESIPAPRGSKDVYVNTSLPEESPSTODGLDSVLPQADSDLD-PGDIAPCCS 902
 QY 809 GDSGMAVGSPSCRIITLPGGLAEOPGAERHESPESLNETORLLLOGLDHPHSCA 868
 DB 903 HKALVAVVDIHDSGRVYL-----ESEGSPTEADYVPLPHESANTASTLTPVGS 956
 QY 869 DASLKMAD 876
 DB 957 AAQLPCAD 964

RESULT 15

B43362
 protein-tyrosine kinase (EC 2.7.1.112) ryk - avian retrovirus RPL30

C:Species: avian retrovirus RPL30
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Feb-1997
 C:Accession: B43362
 R:Jia, R.; Mayer, B.J.; Hanafusa, T.; Hanafusa, H.
 J. Virol. 66, 5975-5987, 1992
 A:Title: A novel oncogene, v-ryk, encoding a truncated receptor tyrosine kinase is transcribed as a env-ryk polypeptide
 A:Reference number: A43362; MID:92407992
 A:Accession: B43362
 A:Molecule type: genomic RNA
 A:Residues: 1-442 <JIA>
 A:Cross-references: GB:M92847
 A:Note: this protein is synthesized as a env-ryk polypeptide
 C:Genetics:
 A:Gene: ryk
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: ATP; autophosphorylation; oncogene; phosphoprotein; phosphotransferase; t
 F:43-318/Domain: protein kinase homology <KIN>
 F:51-59/Region: protein kinase ATP-binding motif
 F:77/Active site: lys & status predicted

Query Match 22.7% Score 1061.5; DB 1; Length 442;
 Best Local Similarity 49.4%; Pred. No. 1.6e-46;
 Matches 217; Conservative 72; Mismatches 125; Indels 25; Gaps 6;

QY 452 VHPAARSRNRRPERIEATLDSIGISDELKEKEDVLIPEOQFTLRMGKGFSGSVRE 511
 DB 511 VHPAARSRNRRPERIEATLDSIGISDELKEKEDVLIPEOQFTLRMGKGFSGSVRE 511

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Db      5 VNYIAKSKYCR---RAVELLTGSLGVSSELOKQKQDVYIDRNALSLCKVLZGEFGSVME 61
QY      512 AQLKOEQGSFYKAVVKMLKADIIASDSIEEFLREACMKKEFDHPHVAKLVGVSLSRAKG 571
Db      62 GRLSQPESTPOKAVAKTKMKDNFNSHRELEEFELSPAACIKDPDHNVATKLGCVCIELSSO- 121
QY      572 RLPIPMVILPFMKHGDHLAFLLASRIGENPENPLQTLIREMYDIACMEYLSRNFIFR 6311
Db      121 QIPKPMVVLPEMKYGDHLSFLRSRLLEAPQFVPLQMLKFMVDIAGMYEYSSROPLHR 180
QY      632 DLARNOMLAEDTVCYADRGSLSKITSGDYIYRQGCASKLPVKMLALESIADNIYTVOSD 691
Db      181 DLARNOMLRDMTVCYADFGSLSKITSGDYIYRGRARAKPVMKIALESIADNYTTKSD 240
QY      692 VMAFGYIMELMTITRGOPFIKAGIENAEIYNTLIGGNRLKOPPECCMEDVYDLMYQWSADPK 751
Db      241 VMAFGYIMELMTITRGMPPIGVQNHIEYETLFIHQRLKRENCIDELDYIMSSCWRAEPA 300
QY      752 QRSFTLRLRELENIILGOLSVLASODPLYNITERAE-----DTAGSLE 797
Db      301 DRPFISOLTKHLEKLTLESLPAPRGSKPIVYVNTSLPESPSDSTQDLGDSVIRQADSDJD 360
QY      798 LPHGDQYYSAGDGSNGGANVGTPSDCRITLITFEGGLAEFGQALEHOPESPJLNTQRLILL 857
Db      361 -PGDIAPCCSHTKAAIYVAVDIHGDGSRVYLESBG--SPTEDAVYPOLP---HEGSAMT 413
QY      858 QOGLLPHSSCADASLKMAD 876
Db      414 EASTLIPVGSLLAOLPCAD 432

```

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 13, 1999, 02:27:10 : Search time 29.27 Seconds

(without alignments)
718.595 Million cell updates/sec

Title: US-09-272-835-20

Perfect score: 4675

Sequence: 1 MCGTAARLGAIVLVIVIGL.....DASLKMADPRFRGNLPLVL 888

Scoring table: BLOSUM62

Searched: 188963 seqs, 23686106 residues

Database: A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2403	51.4	890	1	R7845	Human Rse rprk. Hu
2	2399	51.3	876	1	R60547	Human developmenta
3	2399	51.3	850	1	R60548	Mature human devel
4	2246	48.0	874	1	R60545	Murine development
5	2246	48.0	850	1	R60546	Mature murine deve
6	2239	47.9	880	1	R7846	Mouse Rse rprk. Hu
7	2238	47.9	874	1	W79145	Receptor protein t
8	2238	47.9	874	1	W79145	Receptor protein t
9	1886.5	40.4	887	1	X07286	Human brain-specif
10	1880	40.2	887	1	X07286	Human brain-specif
11	1779	38.1	397	1	W37461	Mouse Ret ligand R
12	1658	35.5	346	1	W37465	A GDNFR-alpha-rela
13	1567	33.5	400	1	W37463	Mouse Ret ligand r
14	1567	33.5	400	1	W37463	Mouse Ret ligand r
15	1567	33.5	400	1	W65116	Human GDNF alpha-3
16	1563	33.4	400	1	W84186	Glial cell line-de
17	1561	33.4	400	1	W84180	A GDNFR-alpha-rela
18	1452	31.1	378	1	W65117	Human GDNF alpha-3
19	1341	28.7	315	1	W37462	Human Ret ligand R
20	1204.5	25.8	894	1	R85753	Human axl receptor
21	1204	25.8	885	1	R85754	Human axl receptor
22	1155.5	24.7	999	1	R87511	Human c-met protoo
23	802	17.2	600	1	R91215	Sperm receptor kin
24	725.5	15.5	847	1	W11941	gd. trkb fusion use
25	718	15.4	814	1	W11940	gd. trkb fusion use
26	717	15.3	850	1	W11942	gd. trkb fusion use
27	682	14.6	172	1	W65118	Human GDNF alpha-3
28	621.5	13.3	489	1	W84298	Consensus sequence
29	618.5	13.2	488	1	W84183	Consensus sequence
30	612.5	13.1	1367	1	R60795	Human IGF-1 recept
31	612.5	13.1	1367	1	R91429	Human type I insul
32	612.5	13.1	1367	1	W37692	Human insulin-like
33	612.5	13.1	1367	1	W54876	Human insulin-like
34	611.5	13.1	1367	1	W54876	Human insulin-like
35	600	12.8	1400	1	R95244	IGF-1 receptor. In
36	597.5	12.8	1370	1	W82791	Human RON receptor
37	587.5	12.6	1370	1	R91430	Rat type I insulin
38	586.5	12.5	1382	1	P60005	Sequence encoded b
39	586	12.5	664	1	R77440	Wild type human in
40	586	12.5	664	1	W71604	Rat neuritin rece
41	586	12.5	464	1	W71602	Rat neuritin rece
42	586	12.5	460	1	W84181	A GDNFR-alpha-rela
43	585.5	12.5	464	1	W92299	Rat GDNFR-beta pol
					W84179	A GDNFR-alpha-rela

ALIGNMENTS

Query Match	Score	DB 1:	Length	890:
Best Local Similarity	96.1%	Pred. No. 3.7e-200;		
Matches 467; Conservative	4;	Mismatches 15;	Indels	0;
Gaps	0;			
Query	382	FSQDADSTFSVVOONSMPARAWPVYGLVLTALYAAALALILRRRRTFRGAF	441	
DB	405	WGQPLVSSHDAAGQGPHSTSNVPLVGLVLTALYAAALALILRRRRTFRGAF	464	
QY	442	DSVMARGEPAVHFRARSFNRPERIATLDSIGISDELKEDVLIPEQOFTLGRML	501	
RESULT	1			
ID	R7845	R7845 standard; Protein; 890 AA.		
AC	R7845;			
DE	01-NOV-1995 (first entry)			
DE	Human Rse rprk.			
KW	RSE; receptor protein tyrosine kinase; rprk; diagnostic; therapy;			
KW	neurodegenerative disease; Alzheimer disease; Parkinson disease;			
OS	Homo sapiens.			
FT	Key	Location/Qualifiers		
FT	peptide	1..40		
FT		/label= Sig_peptide		
FT	modified_site	63		
FT		/label= N-glycosylation_site		
FT	modified_site	191		
FT		/label= N-glycosylation_site		
FT	modified_site	230		
FT		/label= N-glycosylation_site		
FT	modified_site	240		
FT		/label= N-glycosylation_site		
FT	modified_site	293		
FT		/label= N-glycosylation_site		
FT	modified_site	366		
FT		/label= N-glycosylation_site		
FT	modified_site	380		
FT		/label= N-glycosylation_site		
FT	domain	429..451		
FT		/label= Transmembrane_domain		
FT	domain	518..786		
FT		/label= Tyrosine-kinase_domain		
FT		525..530		
FT	binding_site	/label= Mg2+-ATP_binding_site		
FT				
PN	W09514776-A.			
PD	01-JUN-1995.			
PF	15-NOV-1994; U13214.			
PR	23-NOV-1993; US-157563.			
PR	20-DEC-1993; US-170558.			
PR	05-AUG-1994; US-286305.			
PA	(GENE) GENENTECH INC.			
PA	(NEWE) NEW ENGLAND DEACONESS HOSPITAL.			
PI	Godowski PJ, Mark MR, Scadden DT, Sadick MD, Wong WLT;			
DR	WPI; 95-206933/27.			
DR	N-PSDB; Q94421.			
PT	Human and murine receptor protein tyrosine kinase(s) and corresp. DNA -			
PT	for stimulation of cell growth and differentiation e.g. for treatment of			
PT	neurodegenerative and kidney diseases			
PS	Claim 6; Fig.1A; 1199p; English.			
CC	Primers based on conserved sequences from tyrosine kinases were used			
CC	to amplify fragments of tyrosine kinase encoding genes from cDNA			
CC	and a composite sequence, given in Q94421, of a new receptor protein			
CC	tyrosine kinase, Rse, was determined. The extracellular domain of			
CC	RSE is useful therapeutically.			
CC	Sequence 890 AA;			

```

Db 465 DSVMAKGEPAVHFRARASNRPERIEATLDSIGISDELKKEEDVLLPEOQFTLGRML
QY 502 GKGEFSGVREAOIQEDGSEFVAVAKMLKADIIASSDIEEFLEAACKKEFDHPHAKLV
Db 525 GKGEFSGVREAOIQEDGSEFVAVAKMLKADIIASSDIEEFLEAACKKEFDHPHAKLV
QY 562 GVSLSRAKGLPIPMVILPFPMKRGDHAFLASRIENFNLPLQTLIRFMDIACGME
Db 585 GVSLSRAKGLPIPMVILPFPMKRGDHAFLASRIENFNLPLQTLIRFMDIACGME
QY 622 YLSRNFHRLDAAARNCLMADMTVCVADFGLSRKITYSGDYRQGCASKIPVWMLAESL
Db 645 YLSRNFHRLDAAARNCLMADMTVCVADFGLSRKITYSGDYRQGCASKIPVWMLAESL
QY 682 ADNIYTVQSDVMAFGVYTWMEIMTRGQTPYAGINAEIYNILIGNRLKOPPECEMEDVYL
Db 705 ADNIYTVQSDVMAFGVYTWMEIMTRGQTPYAGINAEIYNILIGNRLKOPPECEMEDVYL
QY 742 MYOCMSADPKORPSFTCLRMELNIIQLSVLSASODPLYINIERAEPTAGSLELPGR
Db 765 MYOCMSADPKORPSFTCLRMELNIIQLSVLSASODPLYINIERAEPTAGSLELPGR
QY 802 DQPYSGADGSGMGAVGTPSDCRYLITPGGLAEPQGAHOPESPINETOQLLLQOGL
Db 825 DQPYSGADGSGMGAVGTPSDCRYLITPGGLAEPQGAHOPESPINETOQLLLQOGL
QY 862 LPHSSC 867
Db 885 LPHSSC 890

```

RESULT 2

```

R60547
ID R60547 standard; Protein: 876 AA.
AC R60547;
DT 14-APR-1995 (first entry)
DE Human developmental tyrosine kinase (Dtk).
KW Receptor tyrosine kinase; developmental tyrosine kinase;
KM vertebrate development.
OS Homo sapiens.
PN WO9419463-A.
PD 01-SEP-1994.
PF 16-FEB-1994; NZ0009.
PR 16-FEB-1993; NZ-245917.
PA (AUCK-) AUCKLAND UNISERVICES LTD.
PI Crosier KE, Crosier PS;
DR MPI: 94-294328/36.
DR N-PSDB: 071334.
PT Developmental tyrosine kinase(s) and their ligands - used to
stimulate the proliferation of cells that form part of the CNS
PS Claim 4; Page 60-64; 86pp; English.
CC Dtk is a transmembrane receptor tyrosine kinase whose extracellular
domains contain two immunoglobulin-like motifs followed by two
fibronectin-type III repeats. It is distinguished from RTKs having
CC the equivalently structured extracellular domains by its potential
function based upon its distribution within the mammalian body. (RTK
CC = receptor tyrosine kinase).
SQ Sequence 876 AA;

```

```

Query Match 51.3%; Score 2399; DB 1; Length 876;
Best Local Similarity 95.9%; Pred. No. 8e-200;
Matches 466; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

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```

QY 382 FSDQWADSTESVVOQNSNPMAMWVYLVGVTALVTAALAILLRRRRETRFGQAF 441
Db 391 WSOPLVYSSHDRAQGGPPHSRTSWPVYLVGVTALVTAALAILLRRRRETRFGQAF 450
QY 442 DSVMAGEPAVHFRARASNRPERIEATLDSIGISDELKKEEDVLLPEOQFTLGRML 501
Db 451 DSVMAGEPAVHFRARASNRPERIEATLDSIGISDELKKEEDVLLPEOQFTLGRML 510

```

```

QY 502 GKGEFSGVREAOIQEDGSEFVAVAKMLKADIIASSDIEEFLEAACKKEFDHPHAKLV
Db 511 GKGEFSGVREAOIQEDGSEFVAVAKMLKADIIASSDIEEFLEAACKKEFDHPHAKLV
QY 562 GVSLSRAKGLPIPMVILPFPMKRGDHAFLASRIENFNLPLQTLIRFMDIACGME
Db 571 GVSLSRAKGLPIPMVILPFPMKRGDHAFLASRIENFNLPLQTLIRFMDIACGME
QY 622 YLSRNFHRLDAAARNCLMADMTVCVADFGLSRKITYSGDYRQGCASKIPVWMLAESL
Db 631 YLSRNFHRLDAAARNCLMADMTVCVADFGLSRKITYSGDYRQGCASKIPVWMLAESL
QY 682 ADNIYTVQSDVMAFGVYTWMEIMTRGQTPYAGINAEIYNILIGNRLKOPPECEMEDVYL
Db 691 ADNIYTVQSDVMAFGVYTWMEIMTRGQTPYAGINAEIYNILIGNRLKOPPECEMEDVYL
QY 742 MYOCMSADPKORPSFTCLRMELNIIQLSVLSASODPLYINIERAEPTAGSLELPGR
Db 751 MYOCMSADPKORPSFTCLRMELNIIQLSVLSASODPLYINIERAEPTAGSLELPGR
QY 802 DQPYSGADGSGMGAVGTPSDCRYLITPGGLAEPQGAHOPESPINETOQLLLQOGL
Db 811 DQPYSGADGSGMGAVGTPSDCRYLITPGGLAEPQGAHOPESPINETOQLLLQOGL
QY 862 LPHSSC 867
Db 871 LPHSSC 876

```

RESULT 3

```

R60548
ID R60548 standard; Protein: 850 AA.
AC R60548;
DT 14-APR-1995 (first entry)
DE Mature human developmental tyrosine kinase (Dtk).
KW Receptor tyrosine kinase; developmental tyrosine kinase;
KM vertebrate development.
OS Homo sapiens.
PN WO9419463-A.
PD 01-SEP-1994.
PF 16-FEB-1994; NZ0009.
PR 16-FEB-1993; NZ-245917.
PA (AUCK-) AUCKLAND UNISERVICES LTD.
PI Crosier KE, Crosier PS;
DR MPI: 94-294328/36.
DR N-PSDB: 071335.
PT Developmental tyrosine kinase(s) and their ligands - used to
stimulate the proliferation of cells that form part of the CNS
PS Claim 5; Page 64-67; 86pp; English.
CC Dtk is a transmembrane receptor tyrosine kinase whose extracellular
domains contain two immunoglobulin-like motifs followed by two
fibronectin-type III repeats. It is distinguished from RTKs having
CC the equivalently structured extracellular domains by its potential
function based upon its distribution within the mammalian body. (RTK
CC = receptor tyrosine kinase).
SQ Sequence 850 AA;

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Query Match 51.3%; Score 2399; DB 1; Length 850;
Best Local Similarity 95.9%; Pred. No. 7.6e-200;
Matches 466; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

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QY 382 FSDQWADSTESVVOQNSNPMAMWVYLVGVTALVTAALAILLRRRRETRFGQAF 441
Db 365 WSOPLVYSSHDRAQGGPPHSRTSWPVYLVGVTALVTAALAILLRRRRETRFGQAF 424
QY 442 DSVMAGEPAVHFRARASNRPERIEATLDSIGISDELKKEEDVLLPEOQFTLGRML 501
Db 425 DSVMAGEPAVHFRARASNRPERIEATLDSIGISDELKKEEDVLLPEOQFTLGRML 484
QY 502 GKGEFSGVREAOIQEDGSEFVAVAKMLKADIIASSDIEEFLEAACKKEFDHPHAKLV 561

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Db 485 GGEFGSVREAOIKQEDSSFVAVKMKADIIASSDIEEFLREAAKKEFDHPHAKLV 544
OY 562 GVSLSRAKGRLPIMVILPFMKHGDHLAFLASRIGENPNFLPQTLIRFMDIACME 621
Db 545 GVSLSRAKGRLPIMVILPFMKHGDHLAFLASRIGENPNFLPQTLIRFMDIACME 604
OY 632 YLSRNFTHRDIAARNCLAEADMTVCVADFGLSRKISGDIYRGOCASKLVPVKALLES 681
Db 605 YLSRNFTHRDIAARNCLAEADMTVCVADFGLSRKISGDIYRGOCASKLVPVKALLES 664
OY 662 ADNLYTQSDVMAFGVTMWEIMTRGQTPYAGIENAEIYNILGSRNLRKQPECEMEDYDL 741
Db 665 ADNLYTQSDVMAFGVTMWEIMTRGQTPYAGIENAEIYNILGSRNLRKQPECEMEDYDL 724
OY 742 MYCKMSADPKORPSTFCLRMELNITLGLSVLSASODPLYNIRAEPTAGSLELPGR 801
Db 725 MYCKMSADPKORPSTFCLRMELNITLGLSVLSASODPLYNIRAEPTAGSLELPGR 784
OY 802 DOPYSGAGDSGMAVGSTPDCRYILTPGGLAEQPGCAEHQEPSPINETORLLLOGL 861
Db 785 DOPYSGAGDSGMAVGSTPDCRYILTPGGLAEQPGCAEHQEPSPINETORLLLOGL 844
OY 862 LPHSSC 867
Db 845 LPHSSC 850

```

RESULT 4

```

ID R60545 standard; Protein; 874 AA.
AC R60545;
DE 14-APR-1995 (first entry)
DE Murine developmental tyrosine kinase (Dtk).
KW Receptor tyrosine kinase; developmental tyrosine kinase;
KW vertebrate development.
OS Mus musculus.
PN MO9419463-A.
PD 01-SEP-1994.
PE 16-FEB-1994; NZ-245917.
PR 16-FEB-1993; NZ-245917.
PA (AUCK-) AUCKLAND UNISERVICES LTD.
PI Crosier KE, Crosier PS;
DR WPI: 94-294328/36.
DR N-PSDB: 071332.
PT Developmental tyrosine kinase(s) and their ligands - used to
stimulate the proliferation differentiation or survival of foetal
or adult neuronal cells of cells that form part of the CNS
PS Claim 2; Page 53-57; 86pp; English.
CC Dtk is a transmembrane receptor tyrosine kinase whose extracellular
domains contain two immunoglobulin-like motifs followed by two
CC fibronectin-type III repeats. It is distinguished from RTKs having
CC the equivalently structured extracellular domains by its potential
CC function based upon its distribution within the mammalian body. (RTK
CC = receptor tyrosine kinase).
SQ Sequence 874 AA;

```

```

Query Match 48.0%; Score 2246; DB 1; Length 874;
Best Local Similarity 90.1%; Pred. No. 1.6e-186;
Matches 438; Conservative 14; Mismatches 34; Indels 0; Gaps 0;
OY 382 FSDQMDSTFSVVOOONSNPAMRAWVPVYGVLTALVTAALAILLRKRKRETRGOAF 441
Db 389 WSOPLVYSSHDHAGRGOPPHSRSTSWPVYGVLTALVTAALAILLRKRKRETRGOAF 446
OY 442 DSVNAGEPAVHRRAASFNERPERIEATLDSIGISDELKELDEVLIPEQOFTLGRML 501
Db 449 DSVNAGEPAVHRRAASFNERPERIEATLDSIGISDELKELDEVLIPEQOFTLGRML 508
OY 502 GKGEFGSVREAOIKQEDSSFVAVKMKADIIASSDIEEFLREAAKKEFDHPHAKLV 561
Db 509 GKGEFGSVREAOIKQEDSSFVAVKMKADIIASSDIEEFLREAAKKEFDHPHAKLV 568

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OY 562 GVSLSRAKGRLPIMVILPFMKHGDHLAFLASRIGENPNFLPQTLIRFMDIACME 621
Db 569 GVSLSRAKGRLPIMVILPFMKHGDHLAFLASRIGENPNFLPQTLIRFMDIACME 628
OY 622 YLSRNFTHRDIAARNCLAEADMTVCVADFGLSRKISGDIYRGOCASKLVPVKALLES 681
Db 629 YLSRNFTHRDIAARNCLAEADMTVCVADFGLSRKISGDIYRGOCASKLVPVKALLES 688
OY 682 ADNLYTQSDVMAFGVTMWEIMTRGQTPYAGIENAEIYNILGSRNLRKQPECEMEDYDL 741
Db 689 ADNLYTQSDVMAFGVTMWEIMTRGQTPYAGIENAEIYNILGSRNLRKQPECEMEDYDL 748
OY 742 MYCKMSADPKORPSTFCLRMELNITLGLSVLSASODPLYNIRAEPTAGSLELPGR 801
Db 749 MYCKMSADPKORPSTFCLRMELNITLGLSVLSASODPLYNIRAEPTAGSLELPGR 808
OY 802 DOPYSGAGDSGMAVGSTPDCRYILTPGGLAEQPGCAEHQEPSPINETORLLLOGL 861
Db 809 ERSSSEAGDSGMAVGSTPDCRYILTPGGLAEQPGCAEHQEPSPINETORLLLOGL 868
OY 862 LPHSSC 867
Db 869 LPHSSC 874

```

RESULT 5

```

ID R60546 standard; Protein; 850 AA.
AC R60546;
DE 14-APR-1995 (first entry)
DE Mature murine developmental tyrosine kinase (Dtk).
KW Receptor tyrosine kinase; developmental tyrosine kinase;
KW vertebrate development.
OS Mus musculus.
PN MO9419463-A.
PD 01-SEP-1994.
PE 16-FEB-1994; NZ-245917.
PR 16-FEB-1993; NZ-245917.
PA (AUCK-) AUCKLAND UNISERVICES LTD.
PI Crosier KE, Crosier PS;
DR WPI: 94-294328/36.
DR N-PSDB: 071333.
PT Developmental tyrosine kinase(s) and their ligands - used to
stimulate the proliferation differentiation or survival of foetal
or adult neuronal cells of cells that form part of the CNS
PS Claim 3; Page 57-60; 86pp; English.
CC Dtk is a transmembrane receptor tyrosine kinase whose extracellular
domains contain two immunoglobulin-like motifs followed by two
CC fibronectin-type III repeats. It is distinguished from RTKs having
CC the equivalently structured extracellular domains by its potential
CC function based upon its distribution within the mammalian body. (RTK
CC = receptor tyrosine kinase).
SQ Sequence 850 AA;

```

```

Query Match 48.0%; Score 2246; DB 1; Length 850;
Best Local Similarity 90.1%; Pred. No. 1.5e-186;
Matches 438; Conservative 14; Mismatches 34; Indels 0; Gaps 0;
OY 382 FSDQMDSTFSVVOOONSNPAMRAWVPVYGVLTALVTAALAILLRKRKRETRGOAF 441
Db 365 WSOPLVYSSHDHAGRGOPPHSRSTSWPVYGVLTALVTAALAILLRKRKRETRGOAF 424
OY 442 DSVNAGEPAVHRRAASFNERPERIEATLDSIGISDELKELDEVLIPEQOFTLGRML 501
Db 425 DSVNAGEPAVHRRAASFNERPERIEATLDSIGISDELKELDEVLIPEQOFTLGRML 484
OY 502 GKGEFGSVREAOIKQEDSSFVAVKMKADIIASSDIEEFLREAAKKEFDHPHAKLV 561
Db 485 GKGEFGSVREAOIKQEDSSFVAVKMKADIIASSDIEEFLREAAKKEFDHPHAKLV 544
OY 562 GVSLSRAKGRLPIMVILPFMKHGDHLAFLASRIGENPNFLPQTLIRFMDIACME 621

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Db 545 GVSLSRAKGRLPIMVILPEMKGDLHAFLASRIGENFNLQTLVPMWDIACME 604
QY 622 YLSRNFTHRDLAARNCLAEEDMTVCVADFGLSRKIYSGDYRGGCASKLPVKWLALESL 681
Db 605 YLSRNFTHRDLAARNCLAEEDMTVCVADFGLSRKIYSGDYRGGCASKLPVKWLALESL 664
QY 682 ADNLTYVSDVMAFVGTWMEIMTRGOTPYAGIENAEIYNYLIGGNRLKQPECEMEDVYDL 741
Db 665 ADNLTYVSDVMAFVGTWMEIMTRGOTPYAGIENAEIYNYLIGGNRLKQPECEMEDVYDL 724
QY 742 MYQCSADPKORPSFTCLRMELNITLIGOLSVLSASODPLYNITERAEPTAGSLELPGR 801
Db 725 MYQCSADPKORPSFTCLRMELNITLIGOLSVLSASODPLYNITERAEPTAGSLELPGR 784
QY 802 DQPYGAGDGGSGMAGVGTPSDCRITLTPGGLAEOPGAHOPESPPLNETORLLILOGL 861
Db 785 ERSSESAGDGGSGVAGVGIRPSDSRYIFSPGGLSESPQLEQPESPLENORLLILOGL 844
QY 862 LPHSSC 867
845 LPHSSC 850

RESULT 6
R77846
ID R77846 standard; Protein; 880 AA.
AC R77846;
DT 01-NOV-1995 (first entry)
DE Mouse Rse rPRK.
KW RSE: receptor protein tyrosine kinase; rPRK; diagnostic; therapy;
  neurodegenerative disease; Alzheimer disease; Parkinson disease;
  kidney disease.
OS Mus sp.
FH Key
FH peptide
FT modified_site 1..30 Location/Qualifiers
FT modified_site 53 /label- Sig_peptide
FT modified_site 73 /label- N-glycosylation_site
FT modified_site 181 /label- N-glycosylation_site
FT modified_site 220 /label- N-glycosylation_site
FT modified_site 230 /label- N-glycosylation_site
FT modified_site 283 /label- N-glycosylation_site
FT modified_site 356 /label- N-glycosylation_site
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FT modified_site 419..441 /label- N-glycosylation_site
FT domain 508..775 /label- Transmembrane_domain
FT domain 515..520 /label- Tyrosine_kinase_domain
FT binding_site /label- Mg2+-ATP_binding_site
FT
FT WO9514776-A.
PD 01-JUN-1995.
PD 15-NOV-1994; U13214.
PR 23-NOV-1993; US-157563.
PR 20-DEC-1993; US-170558.
PR 05-AUG-1994; US-286305.
PR (GETH ) GENENTECH INC.
PA (NEMO-) NEW ENGLAND DEACONESS HOSPITAL.
PI Godowski PJ, Mark MR, Scadden DT, Sackick MD, Wong WLT;
  WPI: 95-206933/27.
DR N-PSDB; Q94422.
PT Human and murine receptor protein tyrosine kinase(s) and corresp. DNA -
  for stimulation of cell growth and differentiation e.g. for treatment of
  neurodegenerative and kidney diseases

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PS Claim 6; Fig.1B; 119pp; English.
CC The murine homolog (given in Q94422) of human Rse cDNA (Q94421) was
CC obtd. from a brain cDNA library using the human Rse cDNA as probe.
SQ Sequence 880 AA;

Query Match          47.9%; Score 2239; DB 1; Length 880;
Best Local Similarity 89.9%; Pred. No. 6,5e-166;
Matches 437; Conservative 14; Mismatches 35; Indels 0; Gaps 0;

QY 382 FSDMADSFYSVYQONSPPANRAMPVVLGVTLVTAALATILTRKRETFGQAF 441
Db 395 WSGPLTVSSHDHNRGQPHRSRTSWPVVLGVTLTAALATILTRKRETFGQAF 454
QY 442 DSYMARGEPAVHFRAARSRRRPERIEATLDSLGISDELKEDVLIPEQOFTLGRL 501
Db 455 DSYMARGEPAVHFRAARSRRRPERIEATLDSLGISDELKEDVLIPEQOFTLGRL 514
QY 502 GKGEFVSREAOLOKEDGSFVAVKMLKADIIASSDIIEEFREAACKEDPHVATLY 561
Db 515 GKGEFVSREAOLOKEDGSFVAVKMLKADIIASSDIIEEFREAACKEDPHVATLY 574
QY 562 GVSLSRAKGRLPIMVILPEMKGDLHAFLASRIGENFNLQTLVPMWDIACME 621
Db 575 GVSLSRAKGRLPIMVILPEMKGDLHAFLASRIGENFNLQTLVPMWDIACME 634
QY 622 YLSRNFTHRDLAARNCLAEEDMTVCVADFGLSRKIYSGDYRGGCASKLPVKWLALESL 681
Db 635 YLSRNFTHRDLAARNCLAEEDMTVCVADFGLSRKIYSGDYRGGCASKLPVKWLALESL 694
QY 682 ADNLTYVSDVMAFVGTWMEIMTRGOTPYAGIENAEIYNYLIGGNRLKQPECEMEDVYDL 741
Db 695 ADNLTYVSDVMAFVGTWMEIMTRGOTPYAGIENAEIYNYLIGGNRLKQPECEMEDVYDL 754
QY 742 MYQCSADPKORPSFTCLRMELNITLIGOLSVLSASODPLYNITERAEPTAGSLELPGR 801
Db 755 MYQCSADPKORPSFTCLRMELNITLIGOLSVLSASODPLYNITERAEPTAGSLELPGR 814
QY 802 DQPYGAGDGGSGMAGVGTPSDCRITLTPGGLAEOPGAHOPESPPLNETORLLILOGL 861
Db 815 ERSSESAGDGGSGVAGVGIRPSDSRYIFSPGGLSESPQLEQPESPLENORLLILOGL 874
QY 862 LPHSSC 867
Db 875 LPHSSC 880

RESULT 7
W79145
ID W79145 standard; Protein; 874 AA.
AC W79145;
DT 19-NOV-1998 (first entry)
DE Receptor protein tyrosine kinase (PTK) subtype tyro-3.
KW PTK; receptor; protein tyrosine kinase; brain tissue.
OS Rattus sp.
FN US581516-A.
PD 22-SEP-1998.
PR 02-JUN-1995; 456647.
PR 15-MAY-1992; US-884486.
PR 02-MAY-1994; US-237401.
PR 02-JUN-1995; US-456647.
PA (SALK ) SALK INST BIOLOGICAL STUDIES.
PI Lai CHC, Lemke GE;
  WPI: 98-53039/45.
DR N-PSDB; V53888.
PT Receptor protein tyrosine kinase polypeptide, tyro-3 - preferably
  expressed in brain tissue
PS Claim 3; Columns 33-40; 46pp; English.
CC This represents a novel receptor protein tyrosine kinase (PTK)
CC polypeptide subtype tyro-3. The invention provides polynucleotide
CC sequences encoding novel PTK polypeptide subtypes tyro-1 to tyro-13.
CC The PTK subtypes are found expressed predominantly in the brain tissue.
SQ Sequence 874 AA;

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the protein expressed, and expression products screened for using antibodies against tyrosine kinase epitopes. These subtype sequences can be used for the design of oligonucleotides, for use in amplification reactions to isolate other subtype sequences. These detection protocols are used in the diagnosis of diseases associated with (receptor) PKs. Recombinant vectors expressing the subtypes can be used to treat related diseases e.g. tumours, by introduction of the vectors into skin transplants, then grafting these into the connective tissue of the dermis, thus specifically targeting tumours as the proteins are released from the matrix.

Sequence 874 AA:

Query Match 47.9%; Score 2238; DB 1; Length 874;
Best Local Similarity 89.7%; Pred. No. 7,9e+186;
Matches 436; Conservative 15; Mismatches 35; Indels 0; Gaps 0;

QY	382	FEQPDADSTFSVVOOQNSNPANRANVPVYGLVTLVTAALATILLRKRRETRFGQAF	441
DB	388	WSQPLVSSSHHAGKQGPSPHSTSWPVVLGVTLLITPAALATILLRKRRETRFGQAF	448
QY	442	DSVMAKGEPAYVFAARAFENRPERIATDLSGISDELKEDVLIPEQOFTLGML	501
DB	449	DSVMAKGEPAYVFAARAFENRPERIATDLSGISDELKEDVLIPEQOFTLGRL	508
QY	502	GKGEFVSREAOLKQEDSEFVAVKMLKADIIASSDIEEFLEAKACKEDHPHAKLY	561
DB	509	GKGEFVSREAOLKQEDSEFVAVKMLKADIIASSDIEEFLEAKACKEDHPHAKLY	568
QY	562	GVSLSRAKGRPLPVPVILPPMKHDDLHAFLIASHRIGENPNPLQTLIRFMYDIACME	621
DB	569	GVSLSRAKGRPLPVPVILPPMKHDDLHAFLIASHRIGENPNPLQTLVRFMYDIACME	628
QY	622	YLSSNFIHRLAANCMLEDMTCVADPELSKRISGDIYRGGCAKLEVKYLALESL	681
DB	629	YLSSNFIHRLAANCMLEDMTCVADPELSKRISGDIYRGGCAKLEVKYLALESL	688
QY	682	ADNLTYSODVWAFVYVMEILTRGQTPYAGIENAEIYNYLIGNRILKQPECKEDVYL	741
DB	689	ADNLTYSODVWAFVYVMEILTRGQTPYAGIENAEIYNYLIGNRILKQPECKEDVYL	748
QY	742	MYOCMSADPKRPSFTCLRMELNLTGLSVLSASODPLYINIERAEPTFGGSLTELPGR	801
DB	749	MYOCMSADPKRPSFTCLRMELNLTGLSVLSASODPLYINIERAEPTFGGSLTELPGR	808
QY	802	DQPSGADDSGMANVGSTPDCRYILTPGGLAQPGQAEHQPSPLNETORLLILLOGL	861
DB	809	ERSSSEADDSGVAVGIPDSISRYIFSPGLSESPQGLEQPESSPLNETORLLILLOGL	868
QY	862	LPSSC 867	
DB	869	LPSSC 874	
RESULT	9		
Y07286	ID	Y07286 standard; Protein; 887 AA.	
AC	Y07286;		
DT	06-JUL-1999	(first entry)	
DE	Human brain-specific tyrosine kinase (BTK) protein.		
KM	Human; brain; tyrosine kinase; Btk; drug application; antigen;		
OS	Human sample.		
PN	J08256780-A.		
PD	08-OCT-1996.		
PF	17-MAR-1995; 097411.		
PR	17-MAR-1995; JP-097411.		
PA	(CHUS) CHUGAI PHARM CO LTD.		
WP	WPI; 96-500368/50.		
NR	N-PSDB; X07286.		
FT	Gene coding brain-specific tyrosine kinase - can be used to detect		
PT	nervous skin syndrome related antigen		
DS	Disclosure: Fig 8: 31pp; Japanese		

CC This sequence represent a human brain-specific tyrosine kinase (Btk).
 CC The coding DNA can be used in drug applications, especially to detect
 CC a nervous skin syndrome (sic) related antigen.
 CC Sequence 887 AA:

Query Match 40.4%; Score 1886.5; DB 1; Length 887;
 Best Local Similarity 73.7%; Pred. No. 2.9e-155;
 Matches 345; Conservative 68; Mismatches 42; Indels 13; Gaps 2;

QY 405 AMVYVGLVLAALTAALATLILKRRKRRFGQAPSVARQEPVAFHFAAASFNRR 464
 DB 422 SMVYVGLMIALVSGAALVLAALKRRKRRFGQAFVSQVGRKEPAVHFAAARFNDR 481
 QY 465 PERLEATLDSIGISDELKEKLEDEVLPEOQFTLGRMLKGFSGSVREAOLEKQDGSFVK 524
 DB 482 PERLEATLDSIGISDELKEKLEDEVLPEOQFTLGRMLKGFSGSVREAOLEKQDGSFVK 541
 QY 525 AVKMLKADIIASSPIEFRLRAACKEEDHFAKLVGVSLRSPAKGRPLPVLFPFK 584
 DB 542 AVKIKADIMFSSDIEFFLHAACMKFEDHFAVRLVGVSLRTRAKGRVPLPVLFPFK 601
 QY 585 HCDLHAFILASRIENEFNPLQTLIRFMDIACGMETLSRNFTHDLAARNOM 640
 DB 602 HCDLHAFILASRIENEFNPLQTLIRFMDIACGMETLSRNFTHDLAARNOM 661
 QY 640 ---LAEDMTVCVADFGISRRKITYSGDYRQGCASRLPYKMLTLESLADNLTYSQDVAFG 696
 DB 662 TRGLVEDMTVCVADFGISRRKITYSGDYRQGCASRLPYKMLTLESLADNLTYSQDVAFG 721
 QY 697 VTMWEITRQGTFRAGIENAEIYNYLIGGNRKLKOPPECMEDVDYDLMTQCSADPKRPSF 756
 DB 722 VTMWEITRQGTFRAGIENAEIYNYLIGGNRKLKOPPECMEDVDYDLMTQCSADPKRPSF 781
 QY 757 TCMRETELITGOLSVASODPLYINIERAEPTAGSGISLEPERDPPYGADGSGMGA 816
 DB 782 SCRLVELHNLGOLAITTSQEPYLLINIDRAEPFEPESAPPGADPPYGSGDGATVSG 841
 QY 817 VGGTSPDCRYILTPGGLAEPGOAEOHPESPPLMETORILLQOGLPH 864
 DB 842 MAGGTRECRYLVPAGIGDQPSSEHQRDPFMETQ-----DGVISH 884

RESULT 40
 W37461
 ID W37461 standard; Protein; 397 AA.
 DT 21-MAY-1998 (first entry)
 KW Mouse Ret ligand RetL3.
 KW Ret ligand; RetL; RetL3; receptor; signal transduction; mouse;
 KW kidney growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neurone disease; multiple sclerosis;
 KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
 KW cranial nerve injury; spinal cord injury; Down's syndrome;
 KW cerebral palsy; Lyme disease; muscular dystrophy;
 KW myasthenia gravis; tumour; therapy.
 OS Mus musculus.
 PN W09744356-A2.
 PD 27-NOV-1997.
 PR 10-APR-1997; 007726.
 PR 08-MAY-1996; US-017427.
 PR 07-JUN-1996; US-017427.
 PR 16-JUL-1996; US-019300.
 PR 16-JUL-1996; US-021859.
 PA (BIO) BIOGEN INC.
 PI Cate RL, Hession C, Sanicola-Nedel M;
 DR WPI 98-018431/02.
 N-PSDB: V00249.
 KW New nucleic acid encoding ret receptor ligands and related proteins
 KW -vectors, transformed cells and antibodies, used for promoting cell
 KW growth and improving survival of injured cells, especially renal or
 KW nerve cells

PS Claim 2; Page 77-78; 113pp; English.
 CC This amino acid sequence comprises mouse Ret ligand (RetL) RetL3,
 CC deduced from cDNA clones (see V00249) isolated from an EST
 CC database and by 5'RACE. Rat and human RetL, human RetL2 and RetL3
 CC sequences (see W37457-60 and W37462-63) are also claimed. RetL is
 CC a key component of the Ret signalling pathway that specifically
 CC interacts with Ret receptor protein, triggering Ret dimerisation
 CC and/or autophosphorylation of the Ret tyrosine kinase domain.
 CC Vectors containing RetL3 DNA and prokaryotic or eukaryotic host
 CC cells transformed or transfected with these vectors are claimed, as
 CC well as a method for production of RetL3, its soluble variants and
 CC fusion proteins with a toxin, imageable compound or radionuclide.
 CC RetL3, optionally when expressed from vectors in vivo, is used to
 CC promote growth of new tissue and survival of damaged tissue,
 CC particularly kidney or neural tissue. Typical applications are in
 CC renal failure, nephritis, kidney transplants, toxic or hypoxic
 CC injury, neurodegeneration, motor neurone disease, multiple sclerosis,
 CC bacterial, viral or prion infections (e.g. meningitis, myelopathy
 CC associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
 CC spinal cord injury, developmental disorders such as Down's syndrome
 CC and cerebral palsy, or conditions involving the peripheral nervous
 CC system (Lyme disease, muscular dystrophy and myasthenia gravis).
 CC Fusion proteins are used to deliver toxins etc. to Ret-expressing
 CC cells, especially tumours.
 CC Sequence 397 AA:

Query Match 40.2%; Score 1880; DB 1; Length 397;
 Best Local Similarity 94.1%; Pred. No. 3.1e-155;
 Matches 354; Conservative 5; Mismatches 11; Indels 6; Gaps 1;

QY 54 LEAGSLATENRNVSCQARRKCEANPCKAAOHLGSCISSLRPLPESASADCL 113
 DB 25 LGAGSLATENRNVSCQARRKCEANPCKAAOHLGSCISSLRPLPESASADCL 84
 QY 114 EAAEQLRNSLIDRCRCHRMKHOATCIDTYTVHPARSISGDELVSPEEDVYSKPKM 173
 DB 85 EAAEQLRNSLIDRCRCHRMKHOATCIDTYTVHPARSISGDELVSPEEDVYSKPKM 144
 QY 174 NLSKLMKRPDSDLCKEFMMLCTLDKCDRLKRAYGEACSGIRCOHCLQALRSFEFKA 233
 DB 145 NLSKLMKRPDSDLCKEFMMLCTLDKCDRLKRAYGEACSGIRCOHCLQALRSFEFKA 204
 QY 234 AESHQGLLCCPPEDDCCGERRRNTAPSCALPSVPCNCLDLRSFRADPLCRSLMD 293
 DB 205 AESHQGLLCCPPEDDCCGERRRNTAPSCALPSVPCNCLDLRSFRADPLCRSLMD 264
 QY 294 FQTHGPHMDILGTCAEGRCLRAVILGIGTAMPNPFTSKYNTVYALSCTRGSGNLODE 353
 DB 265 FQTHGPHMDILGTCAEGRCLRAVILGIGTAMPNPFTSKYNTVYALSCTRGSGNLODE 324
 QY 354 CEOLERSFSONCLVEAIAAKKRFHROLFSODMADSTFSVYQOQNSNPAMPAWVVLGV 413
 DB 325 CEOLERSFSONCLVEAIAAKKRFHROLFSODMADSTFSVYQOQNSNPALN-----LQP 378
 QY 414 LRAIVTAALMLILIR 429
 DB 379 RLPIUSFTLPIILQ 394

RESULT 11
 W84182
 ID W84182 standard; Protein; 397 AA.
 AC W84182;
 DT 25-MAR-1999 (first entry)
 DE A GDNFR-alpha-related protein 3 (GRN3).
 KW Rat; glial cell-line derived neurotrophic factor receptor;
 KW GDNFR; glial cell line-derived neurotrophic factor; GDNF;
 KW neurotrophin; signal transduction; dopaminergic nerve cell;
 KW Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;
 KW neurological disorder; diabetes; glaucoma; sensory neuron;
 KW retinal ganglion cell degeneration; sensory neuropathy;
 KW retinopathy; gene therapy; GDNFR-related protein 3; GRN3.

OS Rattus sp.
 PN W09854213-A2.
 PD 03-DEC-1998.
 PE 27-APR-1998: U08486.
 PR 30-MAY-1997: US-866354.
 PA (AMGE-) AMGEN INC.
 PI Fox GM, Jing S, Wen D;
 DR WPI; 99-080806/07.
 DR N-PSDB: V09331.
 PT New isolated glial cell line-derived neurotrophic factor receptors -
 PT used to develop products for treating e.g. improperly functioning
 PT dopaminergic nerve cells, Parkinson's disease, Alzheimer's disease
 PS or amyotrophic lateral sclerosis
 PS Claim 51; Fig 17; 31pp; English.
 CC The present sequence represents a rat glial cell-line derived
 CC neurotrophic factor receptor (GDNFR)-related protein 3 (GRR3).
 CC The protein has similar functions to GDNFR. GDNFR proteins are
 CC functionally characterised by the ability to bind glial cell
 CC line-derived neurotrophic factor (GDNF) and/or neuritin specifically,
 CC and to act as part of a molecular complex which mediates or enhances
 CC the signal transduction affects of GDNF and/or neuritin. The proteins
 CC can be used for treating improperly functioning dopaminergic nerve
 CC cells, Parkinson's disease, Alzheimer's disease or amyotrophic lateral
 CC sclerosis. They can also be used for treating neurological disorders
 CC associated with diabetes, glaucoma or other diseases and conditions
 CC involving retinal ganglion cell degeneration, sensory neuropathy caused
 CC by injury to, insults to, or degeneration of, sensory neurons.
 CC pathological conditions, or disease or injury-related retinopathies.
 CC The products can also be used for detection, diagnosis, drug screening
 CC and gene therapy.
 SQ Sequence 397 AA;

Query Match 38.1%; Score 1779; DB 1; Length 397;
 Best Local Similarity 89.4%; Pred. No. 1.8e-146;
 Matches 336; Conservative 11; Mismatches 23; Indels 6; Gaps 2;

OY 54 LEAGNSLATEENRFVNSTQARKKCEANPACKAAYQHLGSGTSSLSRPLPESAMSADCL 113
 DB 25 LGTGNLSLPENRLVNSTQARKKCEANPACKAAYQHLGSDSTPLSPBSGESATSAACL 84
 OY 114 EAAEOLNSSLIDCRCHRRKHOATCLDIYVTPARSLDYELDYSPEYDVTSSPKMY 173
 DB 85 EAAQOLNSSLIDCRCHRRKHOATCLDIYVTPARSLDYELDYSPEYDVTSSPKMY 144
 OY 174 NLSKIMLKRSDSLCKFALMCTLNDKCDLRAAYGACSGICORHLCLAOIRSEFEKA 233
 DB 145 NLSKIMLKRSDSLCKFALMCTLNDKCDLRAAYGACSGICORHLCLAOIRSEFEKA 204
 OY 234 AESHAOGLLICPCPEDAGCGERRRNTIAPSCALPSTPCLDLRSGCRADPLCRSLMD 293
 DB 205 AESHAOGLLICPCPEDAGCGERRRNTIAPSCALPSTPCLDLRSGCRADPLCRSLMD 264
 OY 294 FQTHCHPMDLIGTCATEQSRLRAVLGLIGTAMTPNFIKSVNTTVALSTCRSGSNLQDE 353
 DB 265 FQTHCHPMDLIGTCATEQSRLRAVLGLIGTAMTPNFIKSVNTTVALSTCRSGSNLQDE 324
 OY 354 CELELESFQNPCLVEAIAAKKRFHQSLSQMDASTFSVVOQNSNPAMRAVPPVGLV 413
 DB 325 CELELESFQNPCLVEAIAAKKRFHQSLSQMDASTFSVVOQNSNPALRP--QLRLPV 382
 OY 414 LVALVTAALALTLR 429
 DB 383 LSEFFI-----LTLLIQ 394

RESULT 12
 ID W37465
 AC W37465 standard; Protein: 346 AA.
 DT 21-MAY-1998 (first entry)
 DE Mouse Ret ligand retL3 partial sequence.
 KW Ret ligand; RetL3; receptor; signal transduction; mouse;

KW cell growth; renal cell; nerve cell; hypoxic injury; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neurone disease; multiple sclerosis;
 KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
 KW cranial nerve injury; spinal cord injury; Down's syndrome;
 KW cerebral palsy; Lyme disease; muscular dystrophy;
 KW myasthenia gravis; tumour; therapy.
 OS Mus musculus.
 PN W09744386-A2.
 PD 27-NOV-1997.
 PE 07-MAY-1997: U07726.
 PR 10-APR-1997: US-017427.
 PR 08-MAY-1996: US-017427.
 PR 07-JUN-1996: US-019300.
 PR 16-JUL-1996: US-021859.
 PA (BIO) BIOGEN INC.
 PI Cate RL, Hession C, Sanicola-Nadel M;
 DR WPI; 98-018431/02.
 DR N-PSDB: V00256.
 PT New nucleic acid encoding ret receptor ligands and related proteins
 PT -vectors, transformed cells and antibodies, used for promoting cell
 PT growth and improving survival of injured cells, especially renal or
 PT nerve cells
 PS Disclosure; Page 73-74; 113pp; English.
 CC This polypeptide comprises a partial sequence of mouse Ret ligand
 CC RetL3, deduced from EST A050083 cDNA (see V00256). A full-length
 CC mouse RetL3 sequence (see W37461) was also obtained. Rat, mouse
 CC and human RetL3, RetL2 and RetL3 cDNA sequences (see V00245-51) and
 CC encoded polypeptides (see W37457-63) are claimed and can be used
 CC in methods for promoting cell growth and improving survival of
 CC cells, especially renal or neural cells.
 SQ Sequence 346 AA;

Query Match 35.5%; Score 1658; DB 1; Length 346;
 Best Local Similarity 93.7%; Pred. No. 4.9e-136;
 Matches 312; Conservative 5; Mismatches 10; Indels 6; Gaps 1;

OY 97 LSRPLPESAMSADCLAEAEOLNSSLIDCRCHRRKHOATCLDIYVTPARSLGDE 156
 DB 17 LSRPLPESAMSADCLAEAEOLNSSLIDCRCHRRKHOATCLDIYVTPARSLGDE 76
 OY 157 LDVSPEDVTSKPMWMLSKMLKPSDCLCKFAMCTLNDKCDLRAAYGACSGIR 216
 DB 77 LDVSPEDVTSKPMWMLSKMLKPSDCLCKFAMCTLNDKCDLRAAYGACSGIR 136
 OY 217 CORHLCLAOIRSEFEKAESHAOGLLICPCPEDAGCGERRRNTIAPSCALPSTPNCID 276
 DB 137 CORHLCLAOIRSEFEKAESHAOGLLICPCPEDAGCGERRRNTIAPSCALPSTPNCID 196
 OY 277 LNSFCRADPLCRSLMDFTCHPMDLIGTCATEQSRLRAVLGLIGTAMTPNFIKSVNT 336
 DB 197 LNSFCRADPLCRSLMDFTCHPMDLIGTCATEQSRLRAVLGLIGTAMTPNFIKSVNT 256
 OY 337 TYALSTCGSGNLDCEQLERSFSONPCLYEALIAAKKRFHQSLSQMDASTFSVVOQ 396
 DB 257 TYALSTCGSGNLDCEQLERSFSONPCLYEALIAAKKRFHQSLSQMDASTFSVVOQ 316
 OY 397 QNSNPAMRAVPPVGLVTAALALTLR 429
 DB 317 QNSNPALR-----LQRLPIILSFTLLPIILQ 343

RESULT 13
 ID W37463
 AC W37463 standard; Protein: 400 AA.
 DT 21-MAY-1998 (first entry)
 DE Human Ret ligand RetL3.
 KW Ret ligand; RetL3; receptor; signal transduction; human;
 KW cell growth; renal cell; nerve cell; renal failure; nephritis;
 KW kidney transplant; toxic injury; hypoxic injury;
 KW neurodegeneration; motor neurone disease; multiple sclerosis;

KW infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
 KW cranial nerve injury; spinal cord injury; Down's syndrome;
 KW cerebral palsy; Lyme disease; muscular dystrophy;
 KW myasthenia gravis; tumour; therapy.
 OS Homo sapiens.
 PN M09744356-A2.
 PD 27-NOV-1997.
 PF 07-MAY-1997; U07726.
 PR 10-APR-1997; US-017427.
 PR 08-MAY-1996; US-017427.
 PR 07-JUN-1996; US-019300.
 PR 16-JUL-1996; US-021859.
 RA (BIOJ) BIOGEN INC.
 PI Cate RL, Hession C, Santicola-Nedel M;
 DR MPI: 98-018431/02.
 NR N-PSDB: V00251.
 PT New nucleic acid encoding ret receptor ligands and related proteins
 PT - vectors, transformed cells and antibodies, used for promoting cell
 PT growth and improving survival of injured cells, especially renal or
 PT nerve cells.
 Claim 2: Page 85-86: 113pp: English.
 This amino acid sequence comprises human Ret ligand (RetL) RetL3,
 deduced from cDNA clones (see V00251) isolated from a adult heart
 and spinal cord libraries. Rat and human RetL1, human RetL2 and
 mouse RetL3 sequences (see W37457-62) are also claimed. Human
 RetL3 is 34.3% identical to human RetL1, 34.9% identical to human
 RetL2 and 76.8% identical to murine RetL3. Ret ligand is a key
 component of the Ret signalling pathway that specifically
 interacts with Ret receptor protein, triggering Ret dimerisation
 and/or autophosphorylation of the Ret tyrosine kinase domain.
 Vectors containing RetL3 DNA and prokaryotic or eukaryotic host
 cells transformed or transfected with these vectors are claimed, as
 well as a method for production of RetL3, its soluble variants and
 fusion proteins with a toxin, imageable compound or radionuclide.
 RetL3, optionally when expressed from vectors in vivo, is used to
 promote growth of new tissue and survival of damaged tissue,
 particularly kidney or neural tissue. Typical applications are in
 renal failure, nephritis, kidney transplants, toxic or hypoxic
 injury, neurodegeneration, motor neurone disease, multiple sclerosis,
 bacterial, viral or prion infections (e.g. meningitis, myelopathy
 associated with HIV or Creutzfeldt-Jakob disease), cranial nerve or
 spinal cord injury, developmental disorders such as Down's syndrome
 and cerebral palsy, or conditions involving the peripheral nervous
 system (lyme disease, muscular dystrophy and myasthenia gravis).
 Fusion proteins are used to deliver toxins etc. to Ret-expressing
 cells, especially tumours.
 Sequence 400 AA;
 SQ

Query Match 33.5%; Score 1567; DB 1; Length 400;
 Best Local Similarity 76.0%; Pred. No. 5e-128;
 Matches 292; Conservative 26; Mismatches 56; Indels 10; Gaps 2;

47 LPVLDLLEAGNSLATENRFVNSCTQARKKCEANPACRAAYOHLGSCSTSLRPLEES 106
 21 LPSPPLPLAAGDPLPTESRLMNSCLQARRKQADPTCSAAHHLDSCSTSLRPLESE 80
 107 AMSADCLAEAOQLNSSLIDRCRHRKHAQATCTDIYTWVHPRASGLDYELDVSPYEDTV 166
 81 SVAPDCLAEAOQLNSSLIDRCRHRKHAQATCTDIYTWVHPRASGLDYELDVSPYEDTV 140
 167 TSKPWNKLSKLNMLKPDSDCLKFAMLCTLDKCDRLRKAYGACSGIRCORHLCLAO 226
 141 TSKPWNKLSKLNMLKPDSDCLKFAMLCTLDKCDRLRKAYGACSGIRCORHLCLAO 200
 227 RSFEKRAEHAAGLLCPCEPDAGCGERRRTIAPSCALSVTPNCLDLRSFCRADPL 286
 201 LTFEKAABEHAAGLLCPCEPDAGCGERRRTIAPSCALSVTPNCLDLRSFCRADPL 260
 287 CSRSLMDFOFHCHPMIDILGTCATQSRCLRAYLGLIGTAMTFNFSKYNTVAALSCTCRG 346
 261 CSRSLMDFOFHCHPMIDILGTCATQSRCLRAYLGLIGTAMTFNFSKYNTVAALSCTCRG 320

QY 347 SGNLDBCEQLERSQNPCLVEAIAAKRFRHQLFSQDMADSTFVSVOQNSNPAMR-- 405
 DB 321 SGNLDBCEQLERSQNPCLVEAIAAKRFRHQLFSQDMADSTFVSVOQNSNPAMR-- 380
 QY 405 AMVPVAVGLTALVTAAALAILL 428
 DB 381 FMVPSLF-----SCLPTILL 396

RESULT 14
 M65116
 ID M65116 standard; Protein; 400 AA.
 AC M65116;
 DT 28-SEP-1998 (first entry)
 DE Human GDNF alpha-3 receptor protein #1.
 KW Glial cell line-derived neurotrophic factor alpha-3 receptor; GDNF;
 KW treatment; neurodegenerative disease; Parkinson's disease; ALS; SMA;
 KW amyotrophic lateral sclerosis; spinal muscular atrophy; nerve; trauma;
 KW Huntington's disease; Alzheimer's disease; diabetic neuropathy; muscle;
 KW muscular dystrophy; diagnostic.
 OS Homo sapiens.
 PI Lawrence GMP;
 DR MPI: 98-29980/27.
 NR N-PSDB: Y35364.
 PT New factor alpha 3 receptor polypeptide and e.g. DNA and agonists -
 PT used to treat neuro degenerative diseases, muscular diseases and
 PT nerve and muscle trauma and in diagnostic assays
 PS Claim 4; Fig 2; 22pp; English.
 CC This sequence represents a novel glial cell line-derived neurotrophic
 CC factor alpha-3 receptor (GDNF alpha-3). This protein can be used to
 CC treat e.g. neurodegenerative diseases (such as Parkinson's disease,
 CC amyotrophic lateral sclerosis (ALS), spinal muscular atrophy (SMA),
 CC Huntington's disease, Alzheimer's disease, diabetic neuropathy),
 CC muscular diseases (including the muscular dystrophies) and nerve and
 CC muscle trauma and in diagnostic assays for such conditions.
 Sequence 400 AA;
 SQ

Query Match 33.5%; Score 1567; DB 1; Length 400;
 Best Local Similarity 76.0%; Pred. No. 5e-128;
 Matches 292; Conservative 26; Mismatches 56; Indels 10; Gaps 2;

QY 47 LPVLDLLEAGNSLATENRFVNSCTQARKKCEANPACRAAYOHLGSCSTSLRPLEES 106
 DB 21 LPSPPLPLAAGDPLPTESRLMNSCLQARRKQADPTCSAAHHLDSCSTSLRPLESE 80
 107 AMSADCLAEAOQLNSSLIDRCRHRKHAQATCTDIYTWVHPRASGLDYELDVSPYEDTV 166
 81 SVAPDCLAEAOQLNSSLIDRCRHRKHAQATCTDIYTWVHPRASGLDYELDVSPYEDTV 140
 167 TSKPWNKLSKLNMLKPDSDCLKFAMLCTLDKCDRLRKAYGACSGIRCORHLCLAO 226
 141 TSKPWNKLSKLNMLKPDSDCLKFAMLCTLDKCDRLRKAYGACSGIRCORHLCLAO 200
 227 RSFEKRAEHAAGLLCPCEPDAGCGERRRTIAPSCALSVTPNCLDLRSFCRADPL 286
 201 LTFEKAABEHAAGLLCPCEPDAGCGERRRTIAPSCALSVTPNCLDLRSFCRADPL 260
 287 CSRSLMDFOFHCHPMIDILGTCATQSRCLRAYLGLIGTAMTFNFSKYNTVAALSCTCRG 346
 261 CSRSLMDFOFHCHPMIDILGTCATQSRCLRAYLGLIGTAMTFNFSKYNTVAALSCTCRG 320
 QY 347 SGNLDBCEQLERSQNPCLVEAIAAKRFRHQLFSQDMADSTFVSVOQNSNPAMR-- 405

DB 321 SGNLDECEMLGEGFHHNCJTEALAKRHFHSQLEFSQDMPHPTFAVMAHONENPAVRPQ 380
 QY 405 AMVPVVLGVLTAALALIL 428
 DB 381 PMVPSLF-----SCTLPIL 396

RESULT 15

W84186
 W84186 standard; Protein; 400 AA.

AC W84186;
 DT 25-MAR-1999 (first entry)
 DE Glial cell line-derived neurotrophic factor receptor gamma 2.
 KW Glial cell line-derived neurotrophic factor; GDNF;
 KW GDNFR-alpha; glial cell line-derived neurotrophic factor; GDNF;
 KW neurodegenerative disease; amyotrophic lateral sclerosis; GDNFR-gamma2;
 KW Parkinson's disease; schizophrenia; insomnia; tardive dyskinesia;
 KW hypertension; pituitary adenomas; hyperprolactinemia; thyroid tumour;
 KW renal disorder; kidney failure; gut dysfunction; regeneration;
 KW cardiomyocyte; epithelium; hepatocyte.
 OS Homo sapiens.
 FH Key
 FT Peptide
 FT 1. 31
 FT /label- signal_peptide
 FT 32. 400
 FT /label- mature_protein
 FT 32. 382
 FT /note- "extracellular domain"
 FT 383. 400
 FT /note- "transmembrane domain"

FT Domain
 FT 383. 400
 FT /note- "transmembrane domain"

PN W09853069-A2.
 PD 26-NOV-1998.
 PE 20-MAY-1998; U10328.
 PR 27-JUN-1997; US-884638.
 PR 20-MAY-1997; US-047092.
 PA (HMA-) HUMAN GENOME SCI INC.
 PI Gentz RL, Hsu T, Ni J, Ruden SM, Young P;
 DR WPI; 99-070150/06.
 DR N-PSDB; V99334.
 PT New isolated glial cell derived neurotrophic factor receptors - used
 PT to develop products for treating e.g. neurodegenerative disorders,
 PT schizophrenia, hypertension, tumours, renal disorders, kidney
 PT failure or gut dysfunction
 PS Claim 53; F1g 7A-D; 156pp; English.
 CC The present sequence represents a glial cell line-derived neurotrophic
 CC factor receptor gamma 2 (GDNFR-gamma2). GDNFR-gamma2 shares high homology
 CC with GDNFR-alpha, which is capable of complexing with glial cell
 CC line-derived neurotrophic factor (GDNF) and mediating cell response to
 CC GDNF. The GDNFR polypeptides and agonists can be used for treating
 CC disorders associated with decreased activity of the respective
 CC polypeptides. They can be used for treating neurodegenerative diseases
 CC such as amyotrophic lateral sclerosis, Parkinson's disease,
 CC schizophrenia, insomnia, tardive dyskinesia, hypertension, pituitary
 CC adenomas, hyperprolactinemia, thyroid tumour, renal disorders, kidney
 CC failure, gut dysfunction, or for regeneration of cardiomyocytes,
 CC epithelium or hepatocytes. Antagonists of the polypeptides can be used
 CC for treating disorders associated with increased activity of the
 CC respective polypeptides. The products can also be used for detection,
 CC diagnosis and drug screening.
 SQ Sequence 400 AA;

Query Match 33.5%; Score 1567; DB 1; Length 400;
 Best Local Similarity 76.0%; Pred. No. 5e-128;
 Matches 292; Conservative 26; Mismatches 56; Indels 10; Gaps 2;

QY 47 LPVLDLLEAGNSLATENRFVNSCTOARKKCEANPACKAYOHLSGCTSSISRLPLEES 106
 DB 21 LPPEPLPLAGDPLPTESRLNLSCLQARKCOADPTCSAYHHLDSCTSSISTPLSEEP 80
 QY 107 AMSADCLAEALQNLNSSLIDCRHRKRAQATCLDIYTVHPARSLGDIYDVSPYEDTV 166

DB 81 SVPADCLPAOOLNNSLSIGCMCHRKNQVACLDIYTVHRAEELGVEYEDVSPYEDTV 140
 QY 167 TSKPWKMLSKLNMKLPDSDCLKFAMLCTLDKCDRLRKAYGEACSGIRGCRHCLQNL 226
 DB 141 TSKPWKMLSKLNMKLPDSDCLKFAMLCTLDKCDRLRKAYGEACSGIRGCRHCLQNL 200
 QY 227 RSFEKKAESHAQGLLCPPEPDAGCGERRRNTIAPSCALPSYTPNCLDLRSFCRADPL 286
 DB 201 LTFEKAEPHAQGLLCPFCAPNDRGCGERRRNTIAPSCALPSYTPNCLDLRSFCRADPL 260
 QY 287 CRSRLMDPOTCHPMDDIGTCATEOSRCLRAYLGLIGTAMPNFIISKYNTVAALSCTCRG 346
 DB 261 CRSRLVDPOTCHPMDDIGTCATEOSRCLRAYLGLIGTAMPNFIISKYNTVAALSCTCRG 320
 QY 347 SGNLDECEMLGEGFHHNCJTEALAKRHFHSQLEFSQDMPHPTFAVMAHONENPAVRPQ 405
 DB 321 SGNLDECEMLGEGFHHNCJTEALAKRHFHSQLEFSQDMPHPTFAVMAHONENPAVRPQ 380
 QY 405 AMVPVVLGVLTAALALIL 428
 DB 381 PMVPSLF-----SCTLPIL 396

Search completed: December 13, 1999, 02:27:16
 Job time: 446 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 13, 1999, 02:45:10 ; Search time 20.22 seconds
(without alignments)
1277.366 Million cell updates/sec

Title: US-09-272-835-20

Perfect score: 4675

Sequence: 1 MGSTAAAGAVILFVYIVGL.....DASIKADPNRFGKDLFVL 888

Scoring table: BLOSUM62

Database: 80000 seqs, 29085965 residues

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2403	51.4	890	1	TYO3_HUMAN	Q06418 homo sapien
2	2257	48.3	880	1	TYO3_RAT	P5146 rattus norv
3	2246	48.0	880	1	TYO3_MOUSE	P5144 mus musculu
4	1200.5	25.7	887	1	UFO_HUMAN	P30520 homo sapien
5	1178.5	25.2	888	1	UFO_MOUSE	Q00993 mus musculu
6	1061.5	22.7	442	1	RK_AVI3	P33497 avian retro
7	646	13.8	370	1	SEA_AVIET	P23049 avian eryth
8	615.5	13.2	1379	1	MET_MOUSE	P16056 mus musculu
9	612.5	13.1	1367	1	IGIR_HUMAN	P08069 homo sapien
10	610	13.0	2554	1	7LES_DROME	P13368 drosophila
11	609.5	13.0	1390	1	IGIR_BOVIN	Q05688 bos taurus
12	606	13.0	1390	1	MET_HUMAN	P08581 homo sapien
13	600	12.8	1400	1	RON_HUMAN	Q04912 homo sapien
14	597.5	12.6	1370	1	IGIR_RAT	P24062 rattus norv
15	590.5	12.6	1115	1	RET_MOUSE	P35546 mus musculu
16	587	12.6	2594	1	7LES_DROI	P08069 homo sapien
17	586.5	12.5	1530	1	ABL_DROME	P00522 drosophila
18	583.5	12.5	1382	1	INSR_HUMAN	P06213 homo sapien
19	582	12.5	1372	1	INSR_MOUSE	P15208 mus musculu
20	579.5	12.4	463	1	NTRR_HUMAN	Q00451 homo sapien
21	576.5	12.4	463	1	NTRR_MOUSE	Q00842 mus musculu
22	576.5	12.3	1383	1	INSR_RAT	P15127 rattus norv
23	575.5	12.3	465	1	NTRR_CHICK	Q13157 gallus gall
24	575	12.3	507	1	KROS_CHICK	P08941 gallus gall
25	574.5	12.3	1114	1	RET_HUMAN	P07949 homo sapien
26	573.5	12.3	1300	1	IRL_CAVPO	P14617 cavla porce
27	570.5	12.2	746	1	ABL_MLVAB	P00521 abelson mur
28	569	12.2	1123	1	ABL_MOUSE	P00520 mus musculu
29	568.5	12.2	402	1	KROS_AVSU	P00529 avian sarco
30	563.5	12.1	1130	1	ABL_HUMAN	P00519 homo sapien
31	563	12.0	2347	1	KROS_HUMAN	P08922 homo sapien
32	559.5	12.0	1268	1	IRR_HUMAN	P14616 homo sapien
33	550.5	11.8	1363	1	ILPR_BRLA	Q02446 brachiolesto
34	547.5	11.7	1053	1	FAK1_RAT	Q13346 rattus norv
35	545.5	11.7	1124	1	TIR2_HUMAN	Q02763 homo sapien
36	544.5	11.6	1052	1	FAK1_HUMAN	Q05397 mus musculu
37	544.5	11.6	1052	1	FAK1_MOUSE	P34152 mus musculu
38	543.5	11.6	1053	1	TIR2_BOVIN	Q00947 gallus gall
39	540.5	11.6	1053	1	FAK1_CHICK	Q13156 gallus gall
40	539	11.5	1122	1	GDNF_MOUSE	Q02888 mus musculu
41	539	11.5	1052	1	FAK1_XENLA	Q01788 xenopus lae
42	536	11.5	1052	1	FAK1_CHICK	P21804 gallus gall
43	535	11.4	819	1	FGRL_CHICK	

ALIGNMENTS

RESULT	1	STANDARD	PRT	890 AA.
TYO3_HUMAN				
AC	006418;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	01-NOV-1997 (Rel. 35, Last annotation update)			
DE	TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (TYROSINE-PROTEIN KINASE RSE) (TYROSINE-PROTEIN KINASE SKY) (TYROSINE-PROTEIN KINASE DTK).			
GN	TYRO3 OR RSE OR SKY OR DTK.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;			
CC	Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 94193774.			
RA	MARK M.R., SCADEN D.T., WANG Z., GU O., GODDARD A., GODDARD P.J.,			
RT	"RSE, a novel receptor-type tyrosine kinase with homology to Axl/Uto,			
RL	is expressed at high levels in the brain."			
RN	J. Biol. Chem. 269:10720-10728(1994).			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 94150991.			
RA	OHASHI K., MIZUNO K., KUMA K., MIYATA T., NAKAMURA T.;			
RT	"Cloning of the cDNA for a novel receptor tyrosine kinase, sky,			
RL	predominantly expressed in brain."			
RN	Oncogene 9:659-705(1994).			
RP	SEQUENCE FROM N.A.			
RX	TISSUE-BRAIN;			
RA	MEDLINE; 95161080.			
RT	CROSIER K.E., HALL L.R., LEWIS P.M., MORRIS C.M., WOOD C.R.,			
RL	MORRIS J.C., CROSSER P.S.;			
RP	"Isolation and characterization of the human DTK receptor tyrosine			
RL	kinase."			
RN	Growth Factors 11:137-144(1994).			
RP	SEQUENCE OF 519-720 FROM N.A.			
RX	MEDLINE; 94085793.			
RA	POLVI A., AMSTRONG E., LAI C., LENKE G., HUBBNER K., SPRITZ R.A.,			
RT	GIJDA L.C., NICHOLS R.D., ALITALO K.;			
RL	"The human TYRO3 gene and pseudogene are located in chromosome			
RL	15q11-q25."			
CC	Gene 134:289-293(1993).			
CC	- FUNCTION: MAY BE INVOLVED IN CELL ADHESION PROCESSES, PARTICULARLY			
CC	IN THE CENTRAL NERVOUS SYSTEM.			
CC	- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	- TISSUE SPECIFICITY: ABUNDANT IN THE BRAIN AND LOWER LEVELS IN			
CC	OTHER TISSUES.			
CC	- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC			
CC	DOMAIN.			
CC	- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.			
CC	- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-TYPE DOMAINS.			
CC	CC This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sdb.ch/announce/			
CC	or send an email to license@isb-sdb.ch).			
DR	EMBL; U05602; AAA19236.1; -			
DR	EMBL; D17517; BAA04467.1; -			
DR	EMBL; U18934; AAC50070.1; -			

44 534.5 11.4 1182 1 ABL2_HUMAN P42684 homo sapien
45 533.5 11.4 1607 1 MIRP_LYMSI Q25410 lymnaea sta

Query Match	Similarity	Score	DB 1	Length
Best Local	96.1%	2403	DB 1	890
Matches	467	Conservative	4	Mismatches 15; Indels 0; Gaps 0
QY	382	FSQOMADSTFSVQOONSNPAMRAWPVYLGVLTALVYAAALAILLRKRKRKEFRGQAF	441	
DB	405	WSQGLVYSSHDRAAGQOGPHSRKSNVPPVYLGVLTALVYAAALAILLRKRKRKEFRGQAF	464	
QY	442	DSVMARGEPAVHRAARSEFNRRPERIEATLTLSLISDELKEKLEDEVLIPEQOFTTGLRL	501	
DB	465	DSVMARGEPAVHRAARSEFNRRPERIEATLTLSLISDELKEKLEDEVLIPEQOFTTGLRL	524	
QY	502	GKGFGSVRAQOLKQEDGSFVYAVYAKMLADIASSDIEEFLRPAACKEFDHPHAKVY	561	
DB	525	GKGFGSVRAQOLKQEDGSFVYAVYAKMLADIASSDIEEFLRPAACKEFDHPHAKVY	584	
QY	562	GVSLRSARKRLPIPVLLPFMKHGDIAFLASLIGENPNPLQTLIRFMDIACGHE	621	
DB	585	GVSLRSARKRLPIPVLLPFMKHGDIAFLASLIGENPNPLQTLIRFMDIACGHE	644	
QY	622	YLSRNFIRHBDLAARCMCLAEDMTVCVADFGLSRKTYGSDYRQGCASKIPVYMLAESI	681	
DB	645	YLSRNFIRHBDLAARCMCLAEDMTVCVADFGLSRKTYGSDYRQGCASKIPVYMLAESI	704	
QY	682	ADNULYVQSDVAAGVYTMELNTRQOTPYAGIENAEIYNYLIGNRLKQPECEMEDYDL	741	
DB	705	ADNULYVQSDVAAGVYTMELNTRQOTPYAGIENAEIYNYLIGNRLKQPECEMEDYDL	764	
QY	742	MYOCMSADRPQRSTFCLEMLNLTIGQLSVLSASQDPLYNIRAEPEPAGSGLELPGR	801	
DB	765	MYOCMSADRPQRSTFCLEMLNLTIGQLSVLSASQDPLYNIRAEPEPAGSGLELPGR	824	
QY	802	DQPSYAGDSGSGAGVGTSPDCRYTLIPGGLAEQPGAEHQEPSPENETORLLLLQOGI	861	
DB	825	DQPSYAGDSGSGAGVGTSPDCRYTLIPGGLAEQPGAEHQEPSPENETORLLLLQOGI	884	

ID	DB	865	LFHSC	890
OY		862	LFHSC	867
Db		865	LFHSC	890
RESULT 2				
TYO3_RAT				
ID	TYO3_RAT	STANDARD:	PRT:	880 AA.
AC	P55146.			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (TYROSINE-PROTEIN KINASE SKT).			
GN	TYRO3 OR SKT.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-BRAIN;			
RX	MEDLINE; 96104999.			
RA	OHASHI K., HONDA S., ICHINOMIYA N., NAKAMURA T., MIZUNO K.;			
RT	"Molecular cloning and in situ localization in the brain of rat sky receptor tyrosine kinase.";			
RL	J. Biochem. 117:1267-1275(1995).			
CC	-1- FUNCTION: MAY BE INVOLVED IN CELL ADHESION PROCESSES, PARTICULARLY IN THE CENTRAL NERVOUS SYSTEM.			
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	-1- TISSUE SPECIFICITY: ABUNDANT IN THE BRAIN AND LOWER LEVELS IN OTHER TISSUES.			
CC	-1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN.			
CC	-1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.			
CC	-1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; D37880; BAA07119.1; ..			
DR	HSSP; P1362; IEG1.			
DR	PFAM; PF00041; fn3; 2.			
DR	PFAM; PF00047; fn3; 2.			
DR	PFAM; PF00069; pkinase; 1.			
DR	PROSITE; PS0107; PROTEIN_KINASE_ATP; 1.			
DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.			
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.			
KW	Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding; Transpherase; Phosphorylation; Transmembrane; Signal; Repeat; Immunoglobulin domain.			
KW	IMMUNOGLOBULIN DOMAIN			
FT	SIGNAL	1	30	POTENTIAL.
FT	CHAIN	31	880	TYROSINE-PROTEIN KINASE RECEPTOR TYRO3.
FT	DOMAIN	31	419	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	420	440	POTENTIAL.
FT	DOMAIN	441	880	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	34	115	IG-LIKE DOMAIN.
FT	DOMAIN	131	200	IG-LIKE DOMAIN.
FT	DOMAIN	214	301	FIBRONECTIN TYPE-III.
FT	DOMAIN	305	401	FIBRONECTIN TYPE-III.
FT	DOMAIN	508	785	PROTEIN KINASE.
FT	NP_BIND	514	522	ATP (BY SIMILARITY).
FT	BINDING	540	540	ATP (BY SIMILARITY).
FT	ACT_SITE	645	645	BY SIMILARITY.
FT	MOD_RES	676	676	PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT	CARBOHYD	53	53	POTENTIAL.
FT	CARBOHYD	75	75	POTENTIAL.
FT	CARBOHYD	181	181	POTENTIAL.

Query Match 48.3%, Score 2257, DB 1, Length 880;
 Best Local Similarity 90.3%, Pred. No. 4.2e-132;
 Matches 439; Conservative 12; Mismatches 35; Indels 0; Gaps 0;

FT	CARBOHYD	220	220	POTENTIAL
FT	CARBOHYD	230	230	POTENTIAL
FT	CARBOHYD	283	283	POTENTIAL
FT	CARBOHYD	356	356	POTENTIAL
FT	CARBOHYD	370	370	POTENTIAL
SO	SEQUENCE	880 AA;	95918 MW;	B77A6F2A CRC32;

RESULT 3
 TYO3_MOUSE STANDARD; PRT: 880 AA.

ID	TYO3_MOUSE	STANDARD	PRT	880 AA.
AC	P55144			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (TYROSINE-PROTEIN KINASE RSE) (TYROSINE-PROTEIN KINASE DTK) (TK19-2)			
DE	TYRO3 OR DTK OR RSE			
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;			
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
RN	[1]			
RN	SEQUENCE FROM N.A.			
RC	TISSUE-BRAIN;			
RC	MEDLINE: 94193774.			
RA	MARK M.R., SCADEN D.T., WANG Z., GU Q., GODDARD A., GODOWSKI P.J.;			
RT	"RSE, a novel receptor-type tyrosine kinase with homology to Ax1/Ufo,			
RL	J. Biol. Chem. 269:10720-10728(1994).			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-BRAIN;			

RE MEDLINE: 95161079.
 RA CROSIER P.S., LEWIS P.M., HALL L.R., VITAS M.R., MORRIS C.M.,
 RA BEIER D.R., WOOD C.R., CROSIER R.E.;
 RT "Isolation of a receptor tyrosine kinase (DTK) from embryonic stem
 RT cells: structure, genetic mapping and analysis of expression";
 RL Growth Factors 11:125-136(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6;
 RX MEDLINE: 94363210.
 RA LAI C., GORE M., LEMKE G.;
 RT "Structure, expression, and activity of Tyro 3, a neural adhesion-
 RT related receptor tyrosine kinase.";
 RL Oncogene 9:2567-2578(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE-BRAIN;
 RX MEDLINE: 95240399.
 RA SCHULZ N., PAULHAC C., LEE L., ZHOU R.;
 RT "Isolation and expression analysis of tyro3, a murine growth factor
 RT receptor tyrosine kinase preferentially expressed in adult brain.";
 RL Brain Res. Mol. Brain Res. 28:273-280(1995).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE-BRAIN;
 RA SAKAKI M.;
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: MAY BE INVOLVED IN CELL ADHESION PROCESSES, PARTICULARLY
 CC IN THE CENTRAL NERVOUS SYSTEM.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: ABUNDANT IN THE BRAIN AND LOWER LEVELS IN
 CC OTHER TISSUES.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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DR	EMBL: U05683; AAA19237.1;	
DR	EMBL: U18933; AAC52148.1;	
DR	EMBL: X78103; CAA54995.1; ALT_INIT.	
DR	EMBL: U18342; AAB26942.1; ALT_INIT.	
DR	EMBL: AB000828; BAA19193.1;	
DR	HSSP: P11362; 1FGI.	
DR	MCD; MG1:104294; TYRO3.	
DR	PFAM: PF00041; fn3; 2.	
DR	PFAM: PF00047; 1g; 2.	
DR	PFAM: PF00069; pkinase; 1.	
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.	
DR	PROSITE: PS00109; PROTEIN_KINASE_TIR; 1.	
DR	PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.	
KW	Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding;	
KW	Transferase; Phosphorylation; Transmembrane; Signal; Repeat;	
KW	Immunoglobulin domain.	
FT	SIGNAL	1..30
FT	CHAIN	31..880
FT	DOMAIN	31..419
FT	TRANSMEM	420..440
FT	DOMAIN	441..880
FT	DOMAIN	34..115
FT	DOMAIN	131..200
FT	DOMAIN	214..301
FT	DOMAIN	305..401
FT	DOMAIN	508..785
FT	NP_BIND	514..522
FT	BINDING	540..540

POTENTIAL.
 TYROSINE-PROTEIN KINASE RECEPTOR TYRO3.
 EXTRACELLULAR (POTENTIAL).
 POTENTIAL.
 CYTOPLASMIC (POTENTIAL).
 IG-LIKE DOMAIN.
 IG-LIKE DOMAIN.
 FIBRONECTIN TYPE-III.
 FIBRONECTIN TYPE-III.
 PROTEIN KINASE.
 ATP (BY SIMILARITY).
 ATP (BY SIMILARITY).

Query Match	25.7%	Score 1200.5; DB 1;	Length 887;
Best Local Similarity	51.18;	Pred. No. 6.4e-67;	

Db 493 RYKSYR---RTTEATLNSLGISEELKEXLRVMDRHKVALGKLGEGEFAVNEGOL 549
 QY 515 KODGSEFVAVYAKMLADITASSDIEFLREAAKMEFDPHVAKLGVLSRAKGRUP 574
 Db 550 MODD-SILKVAKTKMIALCTRESELEFLSEAVCKEFPHPNMRILIGVCGSGDEGPP 608
 QY 575 IPIVILPEPKHGHFLAFLASRIGENPNPLPOTLIRFVNDIACGMEYLSRNFIRDLA 634
 Db 609 EPVILPEPKHGHFLAFLASRIGENPNPLPOTLIRFVNDIACGMEYLSRNFIRDLA 668
 QY 635 ARNCMLAEMTVCAVDFGLSKRIYSGDYRQGCASKLPIVKMLAESLADNLTYSQSDVA 694
 Db 669 ARNCMLNEMNSVCAVDFGLSKRIYSGDYRQGCASKLPIVKMLAESLADNLTYSQSDVA 728
 QY 695 FGVTMMEITRGOTPYAGIENAEIYVILGKRLKQPECEMEDVDYDMYQCSADPKORP 754
 Db 729 FGVTMMEITRGOTPYAGIENAEIYVILGKRLKQPECEMEDVDYDMYQCSADPKORP 788
 QY 755 SFCLMELENITGOLSVLASODPLXINIERA-----EPTAGSGSELGROQFISGACD 810
 Db 789 SFCLMELENITGOLSVLASODPLXINIERA-----EPTAGSGSELGROQFISGACD 844
 Db 811 GSGMAGVGTSPDCRYILTPG-----GLAEQPGCAE 841
 Db 845 SCSCFLAADVHSAAGRYVLCPTAAPTLSADRCGAPRPOED 886

RESULT 6

IRK_AVIR3 STANDARD; PRT: 442 AA.
 AC P33497;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN RYK (EC 2.7.1.112).
 GN V-RYK.
 OS Avian retrovirus RPL30.
 OC Viruses; Retroviral viruses; Retroviridae; Avian type C retroviruses.
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 92407992.
 RA JIA R., MAYER B.J., HANAFUSA T., HANAFUSA H.;
 RT "A novel oncogene, v-ryk, encoding a truncated receptor tyrosine
 RT kinase is transduced into the RPL30 virus without loss of viral
 RT sequences.";
 RL J. Virol. 66:5975-5987(1992).
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
 CC PROTEIN TYROSINE PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: CELL MEMBRANE.
 CC -1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A ENV-RYK
 CC POLIPROTEIN. AN ENV-RYK PRECURSOR FUSION PROTEIN IS FIRST
 CC SYNTHESIZED AND THEN CELLULAR PROTEASE CLEAVES THIS PRECURSOR INTO
 CC GP85 AND THE PUTATIVE ONCOGENE TERMED GP69(GP37-RYK).
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL; M92847; AAA42673.1;
 CC PIR; B43362; B43362.
 CC HSSP; P11362; 1RG1.
 CC PFAM; PF00069; PKINASE.1.
 CC PROSITE; PS00107; PROTEIN_KINASE_ATP.1.
 CC PROSITE; PS00109; PROTEIN_KINASE_TYR.1.
 CC PROSITE; PS50011; PROTEIN_KINASE_DOM.1.
 CC Polyprotein; Transforming protein; Tyrosine-protein kinase;
 CC Transferase; Phosphorylation; ATP-binding; Oncogene; Membrane.

FT DOMAIN 45 316 PROTEIN KINASE.
 FT NP_BIND 51 59 ATP (BY SIMILARITY).
 FT BINDING 77 77 ATP (BY SIMILARITY).
 FT ACT_SITE 181 181 BY SIMILARITY.
 FT MOD_RES 212 212 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 SQ SEQUENCE 442 AA: 49108 MW; 24FD246D CRC32;

Query Match 22.7%; Score 1061.5; DB 1; Length 442;
 Best Local Similarity 49.4%; Pred. No. 1.1e-58;
 Matches 217; Conservative 72; Mismatches 125; Indels 25; Gaps 6;

QY 452 VFERARSEFNERPERIATLSDIGISDELKEKEDVLIPEQOFTLGMKGEGSYRE 511
 Db 5 VNYTAKKSYCR---RAVELTSLGSLVSESLQKQDVVIDRNLALSGVLGEGEGSYME 61
 QY 512 AQLKDEDSFVAVYAKMLADITASSDIEFLREAAKMEFDPHVAKLGVLSRAKRG 571
 Db 62 GRLSQPEGTPOKVAVKTKLNFHSREIEFLSEAVCKEFPHPNMRILIGVCGISGQ- 121
 QY 572 RLPIPVILPEPKHGHFLAFLASRIGENPNPLPOTLIRFVNDIACGMEYLSRNFIR 631
 Db 121 QIPKRVVLPKMKIGDLSFLRSKLEMAPOFVPLQMLKFWVDIALGMEYLSRQFLHR 180
 QY 632 DLAAKNCMLAEMTVCAVDFGLSKRIYSGDYRQGCASKLPIVKMLAESLADNLTYSQSD 691
 Db 181 DLAAKNCMLAEMTVCAVDFGLSKRIYSGDYRQGCASKLPIVKMLAESLADNLTYSQSD 240
 QY 692 VVARGVTMMEITRGOTPYAGIENAEIYVILGKRLKQPECEMEDVDYDMYQCSADPK 751
 Db 241 VVARGVTMMEITRGOTPYAGIENAEIYVILGKRLKQPECEMEDVDYDMYQCSADPK 300
 QY 752 QRPSTCLMELENITGOLSVLASODPLXINIERA-----PRAGSGLE 797
 Db 301 DRPFSQAKVLEKLESLPAPRSGSKDYIVNTSLPESPSTQDLGDSVTPQDSDLD 360
 QY 798 LPRGDPYSGAGSGMAGVGTSPDCRYILPGGLAEQPGCAHOPESPPLNETORLLLL 857
 Db 361 -PGDIAEPCCSHTRKAAVAVDIDHOGSKRYVLESG---SPEDNAVYQLP---HEGSAWT 413
 QY 858 QOGLPHESCADASIKMAD 876
 Db 414 EASTLPVGSLSLAQLPCAD 432

RESULT 7

SEA_AVIR3 STANDARD; PRT: 370 AA.
 AC P23049;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN SEA (EC 2.7.1.112).
 GN V-SEA.
 OS Avian erythroblastosis virus (strain 513).
 OC Viruses; Retroviral viruses; Retroviridae; Avian type C retroviruses.
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89315783.
 RA SMITH D.R., VOGT P.K., HAYMAN M.J.;
 RT "The v-sea oncogene of avian erythroblastosis retrovirus 513: another
 RT member of the protein-tyrosine kinase gene family.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:5291-5295(1989).
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
 CC PROTEIN TYROSINE PHOSPHATE.
 CC -1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A ENV-SEA
 CC POLYPROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE MET TYROSINE KINASE FAMILY OF RECEPTOR.
 CC -----
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 CC -----
 CC EMBL: M25158; E14458; -
 CC PIR: B33902; TVEVSA.
 CC HSSP: P11362; 1FGI.
 CC PRAM: PF00069; PKinase; 1.
 CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE: PS00109; PROTEIN_KINASE_TPR; 1.
 CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 CC Polypeptide: Transforming protein; Tyrosine-protein kinase;
 CC Transferrase; ATP-binding; Oncogene; Phosphorylation.
 CC DOMAIN 60 323 PROTEIN KINASE.
 CC NP_BIND 66 74 ATP (BY SIMILARITY).
 CC BINDING 92 92 ATP (BY SIMILARITY).
 CC ACT_SITE 186 186 BY SIMILARITY.
 CC MOD_RES 216 216 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 CC SEQUENCE 370 AA; 41701 MW; F2E82A14 CRC32;
 CC -----
 CC Query Match 13.8%; Score 646; DB 1; Length 370;
 CC Best Local Similarity 40.3%; Pred. No. 3.8e-33;
 CC Matches 144; Conservative 58; Mismatches 121; Indels 34; Gaps 9;
 CC -----
 CC 432 RKEFRGQADSVARREPAVHFAANSFNERPERLEATVLSIGIDELKEDVLP 491
 CC 8 RPAHFASAGADNAGGSPVLLRTT-----SCLEED-RELLEEVKIDILIP 54
 CC 492 EEOGTL--GNMLKGEFVSREALQKEDGSFVAVYAKMKAQDIASDIEFPEANCM 549
 CC 55 EELILTRSVYIGRNGHSYHYGTMDPLGLNLCIAVKSLSR--TYLEEVFEFLREGITM 113
 CC 550 KEDHPHVAIVGYSLSRSRAGRLPIPVILPEFKHGDILHAFLASRGEPPFPILOTL 609
 CC 114 KGFHHQVLSLLGCL-----PRHGLPLVLPYHRHGDILHFAVAGQ--RSP---TYKEL 163
 CC 610 IRPWVADIACMEYISNFTHRDLAARNCMLAEDMVCVADFGLSRITYSGDY--RQGC 667
 CC 164 IGFGLVALLMEYLAOKFKFHRDLAARNCMLDETLTVVADFGIARVFGREYSINQHR 223
 CC 668 ASLTPYKMLLESADLNYVOSDVAFAVGMVMEIMRGOPFYAGIENALYINLIGNR 727
 CC 224 HALLPYKMLLESLOTOKFTKSDVMSFVLMWELLRGASPYEVDPIYDARLLGRR 283
 CC 728 LKQPPCEMEDVDVLMYCWSADPFRQPSFTCLRMELNITLGOLSVLASQDPLXINI 784
 CC 284 LPQPOPDPFLYGVMLSCMAPTEPERPSFGVGLCELRVLAFL-----EGEYIIM 334
 CC -----
 CC RESULT 8
 CC MET_MOUSE STANDARD; PRT: 1379 AA.
 CC AC P16056; 062125;
 CC DT 01-APR-1990 (Rel. 14, Created)
 CC DT 01-APR-1990 (Rel. 14, Last sequence update)
 CC DT 15-JUL-1998 (Rel. 36, Last annotation update)
 CC DE HEPATOCYTE GROWTH FACTOR RECEPTOR PRECURSOR (MET PROTO-ONCOGENE
 CC TYROSINE KINASE) (EC 2.7.1.112) (HGF-SF RECEPTOR).
 CC MET.
 CC OS Mus musculus (Mouse).
 CC CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC (1)
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE: 88262253.
 CC RA CHAN A.M.L., KING H.W.S., DEAKIN E.A., TEMPEST P.R., HIKKENS J.,
 CC KROELEN V., EDWARDS D.R., WILLS A.J., BROOKES P., COOPER C.S.;
 CC RT "Characterization of the mouse met proto-oncogene."
 CC ONCogene 2:593-599(1988).
 CC (2)
 CC RP SEQUENCE OF 1199-1270 FROM N.A.
 CC RX MEDLINE: 90152381.

RA WILKS A.F., KURBAN R.R., HOVENS C.M., RALPH S.J.;
 RT "The application of the polymerase chain reaction to cloning members
 RT of the protein tyrosine kinase family."
 RL Gene 85:67-74(1989).
 CC -1- FUNCTION: RECEPTOR FOR HEPATOCYTE GROWTH FACTOR. HAS A TYROSINE-
 CC PROTEIN KINASE ACTIVITY.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
 CC PROTEIN TYROSINE PHOSPHATE.
 CC -1- SUBUNIT: HETERODIMER FORMED OF AN ALPHA CHAIN (50 KD) AND A BETA
 CC CHAIN (45 KD) WHICH ARE DISULFIDE LINKED.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- DISEASE: ACTIVATION OF MET AFTER REARRANGEMENT WITH THE TPR
 CC (TRANSLOCATED PROMOTER) LOCUS OF CHROMOSOME 1 PRODUCES AN
 CC ONCOGENIC PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE MET TYROSINE KINASE FAMILY OF RECEPTOR.
 CC -----
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 CC -----
 CC EMBL: Y00671; CA68680.1; -
 CC EMBL: M33424; AAA40015.1; -
 CC PIR: S01254; S01254.
 CC HSSP: P11362; 1FGI.
 CC MCD; MGI196869; MET.
 CC PRAM: PF00069; PKinase; 1.
 CC PRAM: PF01437; Plexin; repeat; 1.
 CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE: PS00109; PROTEIN_KINASE_TPR; 1.
 CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 CC Transferrase; Tyrosine-protein kinase; Proto-oncogene; ATP-binding;
 CC Receptor; Transmembrane; Glycoprotein; Phosphorylation; Signal.
 CC FT CHAIN 25 1379 HEPATOCYTE GROWTH FACTOR RECEPTOR.
 CC FT DOMAIN 25 931 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 932 954 POTENTIAL.
 CC FT DOMAIN 955 1379 CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 1076 1343 PROTEIN KINASE.
 CC FT SITE 306 307 CLEAVAGE (POTENTIAL).
 CC FT NE_BIND 1082 1090 ATP (BY SIMILARITY).
 CC FT BINDING 1108 1108 ATP (BY SIMILARITY).
 CC FT ACT_SITE 1202 1202 BY SIMILARITY.
 CC FT MOD_RES 1233 1233 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 CC FT CARBOHYD 45 45 POTENTIAL.
 CC FT CARBOHYD 106 106 POTENTIAL.
 CC FT CARBOHYD 201 201 POTENTIAL.
 CC FT CARBOHYD 357 357 POTENTIAL.
 CC FT CARBOHYD 358 358 POTENTIAL.
 CC FT CARBOHYD 404 404 POTENTIAL.
 CC FT CARBOHYD 606 606 POTENTIAL.
 CC FT CARBOHYD 634 634 POTENTIAL.
 CC FT CARBOHYD 784 784 POTENTIAL.
 CC FT CARBOHYD 878 878 POTENTIAL.
 CC FT CONFLICT 1159 1159 V -> I (IN REF. 2).
 CC FT CONFLICT 1255 1255 T -> R (IN REF. 2).
 CC FT CONFLICT 1261 1261 K -> T (IN REF. 2).
 CC FT CONFLICT 1269 1270 VL -> IP (IN REF. 2).
 CC SEQUENCE 1379 AA; 153548 MW; E1597F1A CRC32;
 CC -----
 CC Query Match 13.2%; Score 615.5; DB 1; Length 1379;
 CC Best Local Similarity 31.7%; Pred. No. 1.3e-30;
 CC Matches 171; Conservative 80; Mismatches 177; Indels 111; Gaps 21;
 CC -----
 CC 348 GNGDCEQELERFSQNPCLVETAIKMFHQLFSQDAVDSFTS-----VVOQONSAPA 402
 CC DB 877 GN--QSCESLHWHSAGVLTCTVPSDLLKLNSEINI--EKQKAVSYVLGKVIYVDPDON-- 930

[illegible]

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FT CARBOHYD 1889 1889 POTENTIAL.
FT CARBOHYD 1947 1947 POTENTIAL.
FT CARBOHYD 2073 2073 POTENTIAL.
FT VARIANT 392 392 M -> V.
FT VARIANT 1668 1668 M -> V.
FT VARIANT 1703 1703 N -> H.
FT VARIANT 1730 1730 G -> K.
FT VARIANT 1731 1731 G -> E.
FT VARIANT 1741 1741 V -> M.
FT VARIANT 2271 2271 R -> C.
FT CONFLICT 1823 1823 E -> Q (IN REF. 2).
SQ SEQUENCE 2554 AA; 267107 MW; 1143D891 CRC32;

Query Match 13.0%; Score 610; DB 1; Length 2554;
Best Local Similarity 25.8%; Pred. No. 5.9e-30;
Matches 236; Conservative 106; Mismatches 313; Indels 260; Gaps 33;

48 PVLDDLLGNL-----ATENFVNSCTQARKKCEANPACRAAYOHLSGTSLSRP 100
1743 PLGQHLGAGESLNTDLLPFRYVSGILSFYOKRLALPTLVLAPELTLASATPSP 1802
101 LPLESAMSADCLEA-----EQLRNSLIDCRHRMKHQAATCLDIYMTVPARSLGYE 156
1803 RNFESRVLSPRELEVSMLPEOLSES-----VYTLH-----WQOE 1839
157 LDVSPYEDVTISKPKMNLISKLMKLPDSDLCLEFAMLCYLDKCDRIKAYGEACSGIR 216
1840 LDGENVQD-----RREWE-----AHER--RLFTAGTHLTIQK 1870
217 CORHCLAGLSFFPKAESHAQGLLPCPPEDAGCER---RRNTAPSCALPSTYVN 273
1871 -----PSGYSLWQAH-----PYTKSNSESLHVSFAELPELOLELGPY 1913
274 CLDLNFCRADPL-----CSRLLMDPQTHC---HPMDILGCAEQSGRCRAVIGLIGT 324
1914 SLSLWMACTPPPLGSLQLECRSSAQLRRNVAAGHTKAVPELPRTYQCRLLIGYAT 1973
335 AMTPNF-----ISKNTVVALSCGCGSG-----NL 350
1974 PGAPLYHGTAEYETLGDAPSGPKOLEHIAEVEFRTWTAA-----RGNAPIALYNL 2028
331 Q-----DECOLEKRSQNCPLVEA 370
2029 EALQARSDIRRRRRRRNSGSLQELPWAEPPYVEDQMLDFCTTLLS-----CIYKS 2083
371 IAAK-----MRFHROLFSQDMA--DSTFSVOOQNSNPAMRAVYGVLAATYAAALA 424
2084 LHSRLLEFRARSLENGWGPYSESERVAEPYSPKRSGLVALIATAPATVSSCYLA 2143
425 LILKKRRKTRFGOAFDSVARGEPAAVFAARSFNRPERTEATLDSIGIDEL--- 482
2144 LVLVAKVQR-----RLNAKLLQOSRS--TMSNSTLQTOOQMAV 2184
482 -----KELLED--VLIPE--QOFTLGRMLGKGEFGSVRAOLKQEDGSF--VYAVAKL 529
2185 RNRAFSTTSLADIALALPOIMWSQDKLRLFGSSGAFGEVYGQKTEDESEPOFAIKSL 2244
530 KADIIASDIEFLREAAKKEFDHPHAKLVGLVSLNSRARGRLPIPVYLIFPKHGDH 589
2245 RK-----GASEFELLQEOALMNFKNHENVRLVGLCFDTESIS-----LINEHKEAGDL 2295
590 AFLASRI-----GENPNLPLQTLIRPMWDIACGMEYLSSRNFIHDLAARNCMLAD- 644
2296 SYLRAARATSTOEPOPTAGLSELLELAWCIDIYANGCSYLEDMHVRHDLACRNLVTEST 2355
644 -----MTVCYADFGLSKRTISGDIYRGCGASKLPVKMLAESLADNLYTQSVYAFV 697
2356 GSTDRRTVKIGDGLADITKSDYRKREGGLPVKRMSPESLVDGLFTQDSVMAFGV 2415
698 TWEIMTNGQTPYAGIENAEIYNLIGNRLKQDPECEMEDYDLMYQOWASDPQRSFT 757
2416 LCMELITLIGQGPYAAANNFVLAHVKEGRLQDPKCTIKLISLLLCMRIDPERSFR 2475

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QY 758 CLMELENI---LGOLSVLASQD-----PLXINIERAPEPTAGSL- 797
DB 2476 RCYVTLHISTDLRQTQMASTADTVVSCSRPEKVFDFQPLEHNEHNRPDENITL 2535
QY 797 -ELPGRD-QPYSAG 809
DB 2536 REVPLKDKOLYANEG 2550

RESULT 11
IGIR_BOVIN STANDARD; PRT; 640 AA.
AC 005686;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last sequence update)
DE INSULIN-LIKE GROWTH FACTOR I RECEPTOR PRECURSOR (EC 2.7.1.112)
GN (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-KIDNEY;
RX MEDLINE; 92119330.
RA SNEYERS M., KETTMANN R., MASSART S., RENAVILLE R., BURRY A.,
RT PORTETELLE D.;
RT Cloning and characterization of a cDNA encoding the beta-subunit of
RT the bovine insulin-like growth factor-1 receptor.;
RL DNA Seq. 1:405-406(1991)
CC -1- FUNCTION: THIS RECEPTOR BINDS INSULIN-LIKE GROWTH FACTOR I (IGF I)
CC WITH A HIGH AFFINITY AND IGF II WITH A LOWER AFFINITY. IT HAS A
CC TYROSINE-PROTEIN KINASE ACTIVITY.
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
CC PROTEIN TYROSINE PHOSPHATE.
CC -1- SUBUNIT: Tetramer of 2 alpha and 2 beta chains linked by disulfide
CC bonds. The alpha chains contribute to the formation of the ligand-
CC binding domain, while the beta chain carries the kinase domain.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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CC
CC EMBL; X54980; CAA38724.1; -
CC HSP; P06213; IIRK.
CC PRAM; PFO0041; fn3.1.
CC PRAM; PFO0069; pkinase.1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP.1.
CC PROSITE; PS00109; PROTEIN_KINASE_TYR.1.
CC PROSITE; PS00111; PROTEIN_KINASE_DOM.1.
CC TRANSFERASE; Tyrosine-protein kinase; Receptor; Transmembrane;
CC Glycoprotein; ATP-binding; Phosphorylation; Repeat.
CC NON_TER 1 13
CC CHAIN <1 13
CC FT CHAIN 14 640
CC FT CHAIN INSULIN-LIKE GROWTH FACTOR I RECEPTOR,
CC FT CHAIN ALPHA-CHAIN.
CC FT CHAIN INSULIN-LIKE GROWTH FACTOR I RECEPTOR,
CC FT CHAIN BETA-CHAIN.
CC FT DOMAIN 14 208
CC FT DOMAIN 209 232
CC FT DOMAIN 233 640
CC FT DOMAIN 640 101
CC FT DOMAIN EXTRACELLULAR (POTENTIAL).
CC FT DOMAIN CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN FIBRONECTIN TYPE-III.

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FT DOMAIN 102 201 FIBRONECTIN TYPE-III.
FT 272 547
FT NP_BIND 278 286 ATP (BY SIMILARITY).
FT BINDING 306 306 ATP (BY SIMILARITY).
FT ACT_SITE 408 408 BY SIMILARITY.
FT MOD_RES 438 438 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 20 20 POTENTIAL.
FT CARBOHYD 29 29 POTENTIAL.
FT CARBOHYD 37 37 POTENTIAL.
FT CARBOHYD 640 AA: 72511 MW: FD7E7AF7 CRC32:
SQ SEQUENCE

Query Match 13.08; Score 609.5; DB 1; Length 640;
Best Local Similarity 28.2%; Pred. No. 1,3e-30;
Matches 170; Conservative 106; Mismatches 183; Indels 143; Gaps 22;

305 GSGATEOSRCL-----RAYGLIGLTAMP--NFISKVMTVALSTCGSGSLDCEQOLE 358
143 GSGVEDQREVSRQETRYKKGAKLNINPGYTKRIQAT-----SLSGNGS----- 189
359 RSESONPCLVEAIAAKRFRHOLFSDPADSTFVVOQONSPPARAWPVVLGLVLA-- 417
189 -----WIDPVFFVQAKT---YENFIHMLPIAVL 218
417 -LYTAALAILILKRKRKTRFGQAFDSVNAKGPVAFRAKSFNRRERIRATIDSL 475
219 LTVGLGVIMLVFHRKNSRLG---NGVLVAVNPEYFSA----- 258
476 GISDELKEDVLIPE-----QOFTLGRMLKGEFGSGSREAOLK--QEDGSPVAVAK 527
258 -----DYVPEDEWEVAREKTKMSRELQSGSGMYEGVAKVVDDEPTRAIK 306
528 MKRADIIASSDIEEFLREAAKKEFDHPHAKLYGVYLSRANKRLPIPVYILPFMKHD 587
307 TVN-EAASMERIEFLNEASVMKEFNCHVYRLGLVYSOGP-----TLYIMELMTRGD 359
588 LRAFL--LASRIGENPNDP--LOTILRFVNDIACGMEYLSRNFIHRDLAARNCMLAED 643
360 LKSYLRLREPMENNPVLPAPPSLSKMTQAGELADGWAYINANKFVRDLAARNCMAED 419
644 MNYCVADFGSKRTYSGDYRQGCASLTPYKMLAESLADNLTVOSDVNAFGVTMEIM 703
420 FTVKIDFGFTRIYTDYTRKGGKGLLPVRWMSPELSKGVETFDHSDVMSFGVYMEIA 479
704 TGGQFYAGIENAEIYNYLIGNRLOKOPRECMVDYDLMQCSADKORPSF-----TCL 759
480 TLAEPYTGSLNSQVLRVFEVGLDLPDNCPPMLTELMKRCQYKMKRPSLEIITISV 539
760 RMELNIIQLSVLSASQ-----DPLYINIERAE-----EPFA-GGSLLEPGRDQPYSGA 808
540 KDEMAGFREVSYSEENKPRPEPELDELPEMMESVPLDPSASSASLPDR---HSGH 596
809 GGSGGANGVGTSDCRYYITPGGLAEQPOGAHOPESPIN---ETORLLILQOGLPHS 865
597 KAENGSG-----PGVLYLRASFDEROPRYAHNNGRKNERALPLPOS---S 638
866 SC 867
639 TC 640

```

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OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA GIORRANO S.;
RN Submitted (NOV-1990) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 87117655.
RA PARK M.; DEAN M.; KAUL K.; BRAUN M.J.; GONDA M.A.; VANDE WOUDE G.;
RT "Sequence of MET proto-oncogene cDNA has features characteristic of
the tyrosine kinase family of growth-factor receptors."
RL Proc. Natl. Acad. Sci. U.S.A. 84:6379-6383(1987).
[3]
RP SEQUENCE OF 1010-1390 FROM N.A.
RX MEDLINE: 88143699.
RA CHAN A.M.L.; KING H.W.S.; TEMPEST P.R.; DEAKIN E.A.; COOPER C.S.;
RA BROOKES P.;
RT "Primary structure of the met protein tyrosine kinase domain."
RL Oncogene 1:229-233(1987).
[4]
RP SEQUENCE OF 1206-1264 FROM N.A.
RX MEDLINE: 94067791.
RA LEE S.T.; STRUNK K.M.; SPRITZ R.A.;
RT "A survey of protein tyrosine kinase mRNAs expressed in normal human
melanocytes."
RL Oncogene 8:3403-3410(1993).
[5]
RP SEQUENCE OF 1267-1390 FROM N.A.
RX MEDLINE: 86065462.
RA DEAN M.; PARK M.; LE BEAU M.M.; ROBINS T.S.; DIAZ M.O.; ROWLEY J.D.;
RA BLAIR D.G.; VANDE WOUDE G.F.;
RT "The human met oncogene is related to the tyrosine kinase oncogenes."
RL Nature 318:385-388(1985).
[6]
RP SEQUENCE OF 1-754 FROM N.A.
RA PAULEY A.; ANDREWS S.;
RN Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
[7]
RP FUNCTION.
RX MEDLINE: 91118019.
RA BOTTARO D.P.; RUBIN J.S.; FALETTO D.L.; CHAN A.M.-L.; KMECIR T.E.;
RA VANDE WOUDE G.F.; ARONSON S.A.;
RT "Identification of the hepatocyte growth factor receptor as the c-met
proto-oncogene product."
RL Science 251:802-804(1991).
[8]
RP PHOSPHORYLATION AT TYR-1235.
RX MEDLINE: 92011756.
RA FERRACINI R.; LONGATI P.; NALDINI L.; VIGNA E.; COMOGILIO P.M.;
RT "Identification of the major autophosphorylation site of the
Met/hepatocyte growth factor receptor tyrosine kinase."
RL J. Biol. Chem. 266:19558-19564(1991).
[9]
RP VARIANTS HPRC. AND VARIANT VAL-320.
RX MEDLINE: 97285124.
RA SCHMIDT L.; DOH F.-M.; CHEN F.; KISHIDA T.; GLENN G.; CHOYKE P.;
RA SCHERER S.N.; ZHANG Z.; LOBENSKY I.; DEAN M.; ALIKHETS R.;
RA CHIDAMBARAM A.; BERGHEIM U.R.; FELTIS J.T.; CASADEVAL L.C.;
RA ZAMARON A.; BERNDES M.; RICHARD S.; LIPS C.J.M.; WALTHER M.M.;
RA TSUI L.-C.; GEIL L.; ORCUTT M.L.; STACKHOUSE T.; LIPAN J.; SLIFE L.;
RA BRAUCH H.; DECKER J.; NIEHANS G.; HUGHSON M.D.; MOCH H.; STORKEL S.;
RA LERMAN M.I.; LINEHAN W.M.; ZBAR B.;
RT "Germline and somatic mutations in the tyrosine kinase domain of the
MET proto-oncogene in papillary renal carcinomas."
RL Nat. Genet. 16:68-73(1997).
[10]
RP FUNCTION: RECEPTOR FOR HEPATOCYTE GROWTH FACTOR. HAS A TYROSINE-
PROTEIN KINASE ACTIVITY.
[11]
RP CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
PROTEIN TYROSINE PHOSPHATE.
[12]
RP SUBUNIT: HETERODIMER FORMED OF AN ALPHA CHAIN (50 KD) AND A BETA
CHAIN (145 KD) WHICH ARE DISULFIDE LINKED.
[13]
RP SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
[14]
RP DISEASE: ACTIVATION OF MET AFTER REARRANGEMENT WITH THE TPR

```

CC GENE PRODUCES AN ONCOGENIC PROTEIN.
 CC -1- DISEASE: DEFECTS IN MET ARE THE CAUSE OF HEREDITARY PAPILLARY
 CC RENAL CARCINOMA (HPRC). HPRC IS A FORM OF INHERITED KIDNEY CANCER
 CC CHARACTERIZED BY A PREDISPOSITION TO DEVELOP MULTIPLE, BILATERAL
 CC PAPILLARY RENAL TUMORS. THE PATTERN OF INHERITANCE IS CONSISTENT
 CC WITH AUTOSOMAL DOMINANT TRANSMISSION WITH REDUCED PENETRANCE.
 CC -1- SIMILARITY: BELONGS TO THE MET TYROSINE KINASE FAMILY OF RECEPTOR.
 CC
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 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; M35074; AAA59590.1;
 CC EMBL; X54559; -; NOT_ANNOTATED_CDS.
 CC EMBL; J02958; AAA59591.1;
 CC EMBL; AC002080; AAB54047.1;
 CC PIR; A40173; TWEOME.
 CC HSP; P13362; 1FGI.
 CC MIM; 164860;
 CC PFAM; PF00069; PKinase; 1.
 CC PFAM; PF01403; Sema; 1.
 CC DR PFAM; PFO1437; Plexin_Repeat; 1.
 CC DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 CC DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 CC DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 CC KW Transferrase; Tyrosine-protein kinase; Proto-oncogene; ATP-binding;
 CC Receptor; Transmembrane; Glycoprotein; Phosphorylation; Signal;
 CC Chromosomal translocation; Disease mutation; Polymorphism.
 FT SIGNAL 1 24
 FT CHAIN 25 1390
 FT DOMAIN 25 932
 FT TRANSMEM 933 955
 FT DOMAIN 956 1390
 FT NP_BIND 1078 1345
 FT BINDING 1084 1092
 FT ACT_SITE 1110 1110
 FT BINDING 1110 1110
 FT ACT_SITE 1204 1204
 FT SITE 307 308
 FT SITE 1009 1010
 FT MOD_RES 1235 1235
 FT CARBOHYD 45 45
 FT CARBOHYD 106 106
 FT CARBOHYD 149 149
 FT CARBOHYD 202 202
 FT CARBOHYD 399 399
 FT CARBOHYD 405 405
 FT CARBOHYD 607 607
 FT CARBOHYD 635 635
 FT CARBOHYD 785 785
 FT CARBOHYD 879 879
 FT CARBOHYD 930 930
 FT CARBOHYD 930 930
 FT VARIANT 1131 1131
 FT VARIANT 1188 1188
 FT VARIANT 1195 1195
 FT VARIANT 1220 1220
 FT VARIANT 1228 1228
 FT VARIANT 1228 1228
 FT VARIANT 1230 1230
 FT VARIANT 1230 1230
 FT VARIANT 1230 1230

FT FT
 FT VARIANT 1250 1250 /FTID-VAR_006293.
 FT M -> T (IN HPRC; SOMATIC MUTATION).
 FT CONFLICT 755 755 /FTID-VAR_006294.
 FT CONFLICT 1191 1191 S -> STWKEPNTNLSFECFMS (IN REF. 2).
 FT CONFLICT 1191 1191 G -> A (IN REF. 2).
 SQ SEQUENCE 1390 AA; 15526 MW; 650992C2 CRC32;
 Query Match 13.0%; Score 606; DB 1; Length 1390;
 Best Local Similarity 40.1%; Pred. No. 5,2e-30; Matches 129; Conservative 57; Mismatches 114; Indels 22; Gaps 7;
 Db 472 LDSIGSDLEKEDLVLEEQFTL--GRMLGGEFGSYREAOIKQDGSFVAVAKML 529
 1053 IDLSALNPVLQAVOHVIVIPSSLIHFNEVIGHGCGYHGLLNDGKKIKCAVKS 1112
 QY 530 KADIASDIEEFLREACKKEPDHPVAVLVGVLSRAKGRLLPDIWILLPEKRGDLH 589
 Db 1113 NR-ITDIGEVSQFLTEGILINKDFSHPMVLSLIGICLSEGS-----PLVLYLPYKRGDLR 1166
 QY 590 AFLASRIGENPFLPLOTILREAVDIACMEYSSNFTIRDLAANCMLAEDMTYCA 649
 Db 1167 NF-----IRNETHNPYVKDLIGFLOVAKGMKYLASKRFYHDLAARNCMUDEKFTYKVA 1221
 QY 650 DFGISRKIVSGDY--ROGCASKLPEKMLAESLADNLVTVQSDVMAFGVYMEIMTRGO 707
 Db 1222 DFGIARDMYKEYSVYHNKGAFLPYKMALESIQOKFTTKSDVMSFGVYVLEIMTRGA 1281
 QY 708 TPVAGIEMAEIVYVILGGLNFKOPPECMEDVYDMLTQCSADPRKORPSTCLRMELNI 767
 Db 1282 PYPDVATFETITVYLLQGRRLQPEYCPDPLVYMLKCMHPKAMRSPFELVSRISALF 1341
 QY 767 ---LGLSVLASADPLXINIE 785
 Db 1342 STEIGENY---HVNATYVAK 1360
 RESULT 13
 ID RON_HUMAN STANDARD; PRT; 1400 AA.
 AC 004912;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (EC 2.7.1.112)
 DE (MSP RECEPTOR (P185-RON) (CDW136) (CD136 ANTIGEN).
 GN MSTIR OR RON.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-KERATINOCYTES;
 RX MEDLINE; 93241719.
 RA RONSIN C., MUSCATELLI F., MATTEI M.-G., BREATHNACH R.;
 RT "A novel putative receptor protein tyrosine kinase of the met
 RT family";
 RL Oncogene 8:1195-1202(1993).
 RN [2]
 RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
 RX MEDLINE; 96413302.
 RA COLLESI C., SANTORO M.M., GAUDINO G., COMOGGIO P.M.;
 RT "A splicing variant of the RON transcript induces constitutive
 RT tyrosine kinase activity and an invasive phenotype";
 RL Mol. Cell. Biol. 16:5518-5526(1996).
 RN [3]
 RP FUNCTION.
 RX MEDLINE; 95025877.
 RA WANG M.-H., RONSIN C., GESNEL M.-C., COUPEY L., SKEL A.A.;
 RT "Identification of the ron gene product as the receptor for the human
 RT macrophage stimulating protein";
 RL Science 266:117-119(1994).

CC -1- FUNCTION: RECEPTOR FOR MACROPHAGE STIMULATING PROTEIN (MSP). HAS A
 CC TIOSINE-PROTEIN KINASE ACTIVITY.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
 CC PROTEIN TYROSINE PHOSPHATE.
 CC SUBUNIT: HETERODIMER FORMED OF AN ALPHA CHAIN AND A BETA
 CC CHAIN WHICH ARE DISULFIDE LINKED.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC ALTERNATIVE PRODUCTS: AN ALTERNATIVELY SPLICED FORM FOUND IN A
 CC GASTRIC CANCER CELL LINE AND CALLED DELTA-RON, LACKS PART OF THE
 CC EXTRACELLULAR DOMAIN, OLIGOMERIZE AND IS CONSTITUTIVELY ACTIVATED.
 CC -1- TISSUE SPECIFICITY: KERATINOCYTES AND LUNG.
 CC -1- PDB: THE TWO SUBUNITS ARE PROTEOLYTICALLY DERIVED.
 CC -1- PDB: PHOSPHORYLATED IN RESPONSE TO LIGAND BINDING (PROBABLE).
 CC -1- SIMILARITY: BELONGS TO THE MET TYROSINE KINASE FAMILY OF RECEPTOR.
 CC -1- DATABASE: NAME-PROV; NOTE-CD guide cdm136 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdm136.htm".
 CC -----
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 CC or send an email to license@isb-sib.ch).

CC EMBL: X70040; CAA49634.1;
 CC PIR: S31736; S31736.
 CC HSP: P11362; IPI.
 CC MIM: 600168;
 CC DR PRAM: P00069; Pkinase; 1.
 CC DR PRAM: P01403; Sema; 1.
 CC DR PRAM: P01437; Plectin; repeat; 1.
 CC DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 CC DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 CC DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 CC KW Transferrase; Tyrosine-protein kinase; Receptor; Transmembrane;
 CC Glycoprotein; Signal; Phosphorylation; ATP-binding; Polymorphism;
 CC Alternative splicing.
 CC FT SIGNAL 1 24 POTENTIAL.
 CC FT CHAIN 25 1400 MSP RECEPTOR ALPHA CHAIN (POTENTIAL).
 CC FT CHAIN 25 304 MSP RECEPTOR BETA CHAIN (POTENTIAL).
 CC FT DOMAIN 310 1400 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 958 982 POTENTIAL.
 CC FT DOMAIN 983 1400 CYTOPLASMIC (POTENTIAL).
 CC FT BINDING 1088 1345 ATP (BY SIMILARITY).
 CC FT ACT_SITE 1114 1114 ATP (BY SIMILARITY).
 CC FT MOD_RES 1353 1353 BY SIMILARITY.
 CC FT MOD_RES 1360 1360 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 CC FT CARBOHYD 419 419 POTENTIAL.
 CC FT CARBOHYD 458 458 POTENTIAL.
 CC FT CARBOHYD 488 488 POTENTIAL.
 CC FT CARBOHYD 654 654 POTENTIAL.
 CC FT CARBOHYD 720 720 POTENTIAL.
 CC FT CARBOHYD 841 841 POTENTIAL.
 CC FT CARBOHYD 897 897 POTENTIAL.
 CC FT VARSLIC 322 322 MISSING (IN DELTA-RON).
 CC FT VARIANT 322 322 O -> R.
 CC SEQUENCE 1400 AA; 152227 MW; E1322777A CRC32;
 CC -----

Query Match 12.88; Score 600; DB 1; Length 1400;
 Best Local Similarity 27.7%; Pred. No. 1.2e-29;
 Matches 216; Conservative 98; Mismatches 253; Indels 212; Gaps 34;

DB 80 NPACKAYOHLSGTSLSRPLPESAMADCEADQRLNSLIRCHRRKRGATC 139
 776 SPWCGYINSHITIGGHLTSAMHL-----VLSFHDGR--AVESRCEROLPEOOLC 824

QY 140 -LDIY-----WVHPARSLGD-----YELDVSPEEDYTSKPMKNLSKLMK 182
 DB RLPEVYVDDPGWVAGNISARGDGAAGTLTGFRPLPPPPSSNLV-----LK 874
 QY 183 PDSDCLEFAM--LCTHDKDRLRKAYGEACSGIRCOHICLAQLNSFEKAESHAOG 240
 DB 875 PE-EHAIFETIGLGAAYD--CVGINVTG-----GESCOHE-----RGD 912
 QY 241 LLCCGCP-----EDAGGERRNTIAPSCALPSVTNPCLDLRSFCRADPLCRSLMDFO 295
 DB 913 MYVCEPLPSLQLGDDG-----AP-----LQVCV-----937
 QY 296 THCHPDILGTC-----ATROSCRLAYDLIGTAMTPNISKNVTVALSTCRGS-- 348
 DB 937 GECH--ILGRVVRPGDGVOSTLGLPL-----LVAALALALVFSYWRKOL 987
 QY 348 --GNLDECEQLERFSQSNPCLEVALAKRFRROLFSQDMASTFSVVOQNSPAMR 404
 DB 988 VLPPLAND--LASLDQTGATPLPLTLYSGSDYRSGLALPAIDGDSITCVIGASFSDE 1046
 QY 405 AWPVYVGLVLTALYTAALALILLRKRKRETRFGQAFDSVYARGEPAVHRAARFNR 464
 DB 1047 SCVP-----LIRK-----ESIQLR-----1061
 QY 465 PEREATDLSIGIDELKEDVDLIDEOQFTL--GMLKKGEGSVREAOIKOEDGSFV 522
 DB 1061 -----DLDS-----ALAEKVDLIPHERVYTHSDVIRKGGVYVHEGYDOANRI 1109
 QY 523 KVAVKMLKADLIASSDIEEFLENAACKKEFDHPVAKLVGSLSRAKGRPLIPVILTF 582
 DB 1110 QCAIKSL--SRITEMQVYEAFLREGLMRGHNHVVALIIGIMLPES-----LPHVILPY 1163
 QY 583 MKHDDLAFLLASRIGENPNPLQLIIRVWDIACMEYLLSNFIHRDLAARNCMLAE 642
 DB 1164 MCHDDLQFIKSPQ--BNP--TVKDLISFGLQVARGMEYLAQKFEVHRLAARNCMLDE 1218
 QY 643 DMTCVADDFGLSRRTYSGDY--RQGSASLTPYKMLAESLADNLYVQSDVYAFGYTM 700
 DB 1219 SFTYKADDFGLARLDIREYTSVOQHNRHARLPKMAWLESQYTRFTKSDVWSFGYLM 1278
 QY 701 EIMRTGTPAGIENAIYVLLIGNRLKOPPECEMEDYVILANTOCNAGADKORPSFCLR 760
 DB 1279 ELIRGAPPRPHIDPPLTHFLIAGGRLLPPEYCPDLSYVMOQCNEADYAVPTFRVLV 1338
 QY 761 MELENILIGQLSVLASQDP--LYINI-----ERAEEPTAGSLPLP--RDOPYS 806
 DB 1339 GEVQIYVALLGHYVQLPATYMLNLPSTSHENMYVRECPQFS--PMPEGNVAPRPLS 1394

RESULT 14
 ID IGIR_RAT STANDARD; PRT; 1370 AA.
 AC P24062;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE INSULIN-LIKE GROWTH FACTOR I RECEPTOR PRECURSOR (EC 2.7.1.112).
 GN IGIR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RA DU J., DELAFONTAINE P.;
 RL Submitted (MAR-1994) to the EMBL/Genbank/DBD databases.
 RN [2]
 RP SEQUENCE OF 1-364 FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY;
 RX MEDLINE; 90017496.
 RA WERNER H., WOLOSCHAK M., ADAMO M., SHEN-ORR Z., ROBERTS C.T. JR.,
 RA LEROITH D.;
 RT "Developmental regulation of the rat insulin-like growth factor I

"cDNA cloning of mouse ret proto-oncogene and its sequence similarity to the cadherin superfamily";
 RT Oncogene 8:1087-1091(1993).
 CC -1- FUNCTION: PROBABLE RECEPTOR WITH TYROSINE-PROTEIN KINASE ACTIVITY;
 CC IMPORTANT FOR DEVELOPMENT.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
 CC PROTEIN TYROSINE PHOSPHATE
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN PERIPHERAL NERVE CELLS AND
 CC HEMATOPOIETIC CELLS.
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EMBL: X67812; CAA48013.1;
 UN PIR: S2926; S2926.
 DR HSP: P1362; IAGW.
 DR MGD: MGI:97902; RET.
 DR PFAM: PF00028; cadherin.1.
 DR PFAM: PF00068; Kinase.1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR.1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
 KW Transferrase; Tyrosine-protein kinase; ATP-binding; Proto-oncogene;
 KM Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 28 POTENTIAL.
 FT CHAIN 29 1115 PROTO-ONCOGENE TYROSINE-PROTEIN KINASE
 FT DOMAIN 29 637 RECEPTOR RET.
 FT TRANSMEM 638 659 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 660 1115 CYTOPLASMIC (POTENTIAL).
 FT NP_BIND 731 739 ATP (BY SIMILARITY).
 FT BINDING 759 759 ATP (BY SIMILARITY).
 FT ACT_SITE 875 875 BY SIMILARITY.
 FT CARBOHYD 89 89 POTENTIAL.
 FT CARBOHYD 98 98 POTENTIAL.
 FT CARBOHYD 151 151 POTENTIAL.
 FT CARBOHYD 156 156 POTENTIAL.
 FT CARBOHYD 199 199 POTENTIAL.
 FT CARBOHYD 345 345 POTENTIAL.
 FT CARBOHYD 360 360 POTENTIAL.
 FT CARBOHYD 378 378 POTENTIAL.
 FT CARBOHYD 396 396 POTENTIAL.
 FT CARBOHYD 430 430 POTENTIAL.
 FT CARBOHYD 470 470 POTENTIAL.
 FT CARBOHYD 556 556 POTENTIAL.
 SO SEQUENCE 1115 AA; 123728 MW; 089A938E CRC32;

Query Match 12.6%; Score 590.5; DB 1; Length 1115;
 Best Local Similarity 27.4%; Pred. No. 3.6e-29;
 Matches 185; Conservative 107; Mismatches 220; Indels 163; Gaps 26;

QY 249 EDAGCGRRRTTTPSCALPSVYNCIDLRSFCRADPLCRSLMD-----FQTHCHPM 301
 DB 513 EYVGCPK-----SCAVNKRRECECGGSGPTGRCEWROGDGKGTNNFST-CSPS 563
 QY 302 DIL---STCATEQSR-----CLRAYLIGLTAMTPNFISKVNTYVALSCTCRSGSNTL 350
 DB 564 TRCPDGHCAVERSDANICQDCLRA--DIVG-----GHE 597
 QY 351 QDECEQLERSFSONPCLVEALIAAKRFRHOLFSDWADSTFVYQOONSFPAMRAWV-PV 409
 DB 598 RGEROGIKAGYICNCFD-----EKRCFCE-----PEDSGPLCDALCRTI 639
 QY 410 VLGVTALVTAALALILLRKRKRTFGCAFDVMAAGEPAVHFRAARSPNRRPERIE 469

DB 640 ITALFSLIILSIFCVCHHNRHGNRPPIASAEWTFCRPAQGFPISSSGTRRPSLD 699
 QY 470 AT-----LDSLGISDELKERKEDLVLPQOFTLGRMLGKGFEGSVREA---QLKQEDGSE 521
 DB 700 STENVPYDPSKRIEDPKWE-----FPKNIYLKRTTJGEGFEFVYATAPRLGRG-y 753
 QY 522 VKVAVKMLKADIASSDIEFLREACKEEDHPHVAKYVSVLSRAKGRPLIPMYLLP 581
 DB 754 TVAVKXIKEN-ASQSELDRLSEFNILKOVNHPHVIKLYACQSD---GPL---LLIVE 806
 QY 582 FMKHDHLAFILASR-IG-----ENPN--LPLOTLLREMYDIAGMEYL 623
 DB 807 YAKGSLNGFLRDSRKIGPAYVSGGSRNSSLDPHERVLTMDLISFAWQISRGMYL 866
 QY 624 SSRNFIHDLAARNCMAEDMTVCADRGLSRKIYSGDYVNOGASRLPYKWLALLESAD 683
 DB 867 AEMLVHDLAARNILVAEGKKKISDFGLSRDYEEDSVYKSKRGRIPVKMMALTESLFD 926
 QY 684 NLTYVQSDVNAFGVYTMELMTRGOTPYAGIENAEIYVLLIGNRLKOPPECMEDVDLMT 743
 DB 927 HITTQSDVWSFGLVMEIYVLTGNNPYPGIPEPLFNILKTGHRMERPNDCSEMYRLMT 986
 QY 744 QCVSADPKQPSFTCLNRELENNILGQLSVLASODPLYINIERAEPTAGSLELPGRDQ 803
 DB 987 QCVKQEPDKRPFVADISKDEKMAVK-----SRD--YLDL----- 1020
 QY 804 PYSGAGDSGMAVGATPSDPCRYILTPGGLAEQPGQAEHQPESEPLNFTORILLLOGLLP 863
 DB 1020 -----AASPSDS--LLYDGLSEE-----ETPLVDCNNAPLPRS--LP 1054
 QY 864 HSCADASLKMAADPN 878
 DB 1055 STWLENKLYGMSDN 1069

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